

GenCore version 5.1.4_p5_4578
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OK nucleic - nucleic search, using sw model

Run on: February 22, 2003, 04:06:26 : Search time 65.4172 Seconds
(without alignments)
4209.836 Million cell updates/sec

Title: US-09-832-320-1

Perfect score: 898
Sequence: 1 ctgcacgcacgtcgcacgtc.....aaaaaaaaaaaaaaaaaaaaa 898

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 441362 seqs, 153338381 residues

Word size : 25

Total number of hits satisfying chosen parameters: 2779

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

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6: /cgn2_6/p/ptodata/1/ina/backfileseq1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	43	4.8	1483	4 US-09-262-749-1	Sequence 1, Appl
2	43	4.8	1821	4 US-09-149-476-90	Sequence 90, Appl
3	43	4.8	1835	4 US-09-485-549-1	Sequence 1, Appl
4	42	4.7	740	2 US-08-713-000-8	Sequence 8, Appl
5	42	4.7	740	2 US-08-975-316-8	Sequence 8, Appl
6	42	4.7	740	4 US-09-211-710-8	Sequence 8, Appl
7	42	4.7	740	4 US-09-615-192A-8	Sequence 8, Appl
8	42	4.7	741	2 US-08-975-316-58	Sequence 58, Appl
9	42	4.7	741	4 US-09-615-192A-58	Sequence 58, Appl
10	42	4.7	788	4 US-09-615-192A-96	Sequence 96, Appl
11	42	4.7	1315	4 US-09-721-822A-10	Sequence 10, Appl
12	42	4.7	1776	3 US-08-655-352-10	Sequence 10, Appl
13	42	4.7	1776	4 US-09-258-016-10	Sequence 10, Appl
14	42	4.7	1776	4 US-09-257-825B-10	Sequence 10, Appl
15	42	4.7	1824	3 US-08-606-505B-1	Sequence 1, Appl
16	42	4.7	1824	4 US-09-616-990-1	Sequence 1, Appl
17	42	4.7	2399	4 US-09-385-801-1	Sequence 1, Appl
18	41	4.6	347	1 US-08-104-072B-2	Sequence 2, Appl
19	41	4.6	350	1 US-08-171-385-14	Sequence 14, Appl
20	41	4.6	350	3 US-08-361-441B-14	Sequence 14, Appl
21	41	4.6	593	4 US-09-385-982-262	Sequence 262, App
22	41	4.6	958	2 US-08-757-046A-5	Sequence 5, Appl
23	41	4.6	958	3 US-09-447-208-5	Sequence 5, Appl
24	41	4.6	958	3 US-09-135-988-5	Sequence 5, Appl
25	41	4.6	958	4 US-09-277-716-5	Sequence 5, Appl
26	41	4.6	958	4 US-08-597-274A-5	Sequence 5, Appl
27	41	4.6	958	4 US-08-908-909-5	Sequence 5, Appl

28	41	4.6	958	4 US-09-609-161B-5	Sequence 5, Appl
29	41	4.6	958	4 US-08-990-103-5	Sequence 5, Appl
30	41	4.6	1075	4 US-08-400-006B-6	Sequence 6, Appl
31	41	4.6	1143	4 US-09-149-476-119	Sequence 119, App
32	41	4.6	1212	4 US-09-182-145-34	Sequence 34, Appl
33	41	4.6	1212	4 US-09-182-145-35	Sequence 35, Appl
34	41	4.6	1522	4 US-09-413-574-1	Sequence 1, Appl
35	41	4.6	1637	3 US-08-852-824-3	Sequence 3, Appl
36	41	4.6	1728	3 US-08-985-950-7	Sequence 7, Appl
37	41	4.6	1872	4 US-09-801-052-1	Sequence 1, Appl
38	41	4.6	2002	4 US-09-819-993-1	Sequence 1, Appl
39	41	4.6	2196	4 US-09-149-476-163	Sequence 163, App
40	41	4.6	2625	4 US-09-245-041-18	Sequence 18, Appl
41	41	4.6	2671	6 5168051-9	Patent No. 5168051
42	41	4.6	2836	3 US-08-747-221B-24	Sequence 24, Appl
43	41	4.6	2836	3 US-08-747-221B-26	Sequence 26, Appl
44	41	4.6	2836	4 US-09-005-051-24	Sequence 24, Appl
45	41	4.6	2836	4 US-09-005-051-26	Sequence 26, Appl

ALIGNMENTS

RESULT 1

US-09-262-749-1
; Sequence 1, Application US/09262749
; Patent No. 6261793

GENERAL INFORMATION:

APPLICANT: Whyte, David

APPLICANT: McGulick, Marlie

APPLICANT: Nunez-Oliva, Irma

APPLICANT: Hockenderry, Tish

APPLICANT: Pal, James

TITLE OF INVENTION: RAS CONVERTING ENDOPROTEASE (RCE) AND

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSEE: Schering-Plough Corporation

STREET: 2000 Galloping Hill Road K-6-1-1990

CITY: Kenilworth

STATE: New Jersey

COUNTRY: USA

ZIP: 07033

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Power Macintosh

OPERATING SYSTEM: MACOS

SOFTWARE: Microsoft word

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/262,749

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Thampoe, Immac J

REGISTRATION NUMBER: 36,322

REFERENCE/DOCKET NUMBER: OC01005

TELECOMMUNICATION INFORMATION:

TELEPHONE: (908) 298-5061

TELEFAX: (908) 298-5388

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 1483 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: Homo sapiens

FEATURES:

NAME/KEY: CDS

LOCATION: 14..1000

SEQUENCE CHARACTERISTICS:
LENGTH: 740 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-713-000-8

Query Match 4.7%; Score 42; DB 2; Length 740;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 857 GGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 898
|||||
DB 689 GGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 730

RESULT 5
US-08-975-316-8
Sequence 8, Application US/08975316
Patent No. 5952486

GENERAL INFORMATION:
APPLICANT: BLOKSBERG, Leonard N., HAVUKKALA, Ilkka
APPLICANT: and GRIERSON, Alastair W.
TITLE OF INVENTION: MATERIALS AND METHODS FOR
TITLE OF INVENTION: THE MODIFICATION OF PLANT LIGNIN CONTENT
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Law Offices of Ann W. Speckman
STREET: 2601 Elliott Avenue, Suite 4185
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98121

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/975,316
FILING DATE:

CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/713,000
FILING DATE: September 11, 1996
ATTORNEY/AGENT INFORMATION:
NAME: SLEATH, Janet
REGISTRATION NUMBER: 37,007
REFERENCE/DOCKET NUMBER: 11000/1003C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-269-0565
TELEFAX: 206-269-0563
TELEX:

INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 740 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-975-316-8

Query Match 4.7%; Score 42; DB 2; Length 740;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 857 GGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 898
|||||
DB 689 GGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 730

RESULT 6
US-09-211-710-8
Sequence 8, Application US/09211710A

Patent No. 6204434
GENERAL INFORMATION:
APPLICANT: Bloksberg, Leonard N.
APPLICANT: Havukkala, Ilkka
APPLICANT: Grierson, Alastair
TITLE OF INVENTION: Materials and Methods for the
TITLE OF INVENTION: Modification of Plant Lignin Content
FILE REFERENCE: 11000.1003C3
CURRENT APPLICATION NUMBER: US/09/211,710A
CURRENT FILING DATE: 1998-12-14
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 8
LENGTH: 740
TYPE: DNA
ORGANISM: Pinus radiata
US-09-211-710-8

Query Match 4.7%; Score 42; DB 4; Length 740;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 857 GGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 898
|||||
DB 689 GGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 730

RESULT 7
US-09-615-192A-8
Sequence 8, Application US/09615192A
Patent No. 6410718

GENERAL INFORMATION:
APPLICANT: Bloksberg, Leonard N.
APPLICANT: Havukkala, Ilkka
TITLE OF INVENTION: Materials and Methods for the
TITLE OF INVENTION: Modification of Plant Lignin Content
FILE REFERENCE: 11000.1003C4U
CURRENT APPLICATION NUMBER: US/09/615,192A
CURRENT FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 08/975,316
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: US 08/713,000
PRIOR FILING DATE: 1996-09-11
PRIOR APPLICATION NUMBER: US 09/169,789
PRIOR FILING DATE: 1998-10-09
NUMBER OF SEQ ID NOS: 405
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 8
LENGTH: 740
TYPE: DNA
ORGANISM: Pinus radiata
US-09-615-192A-8

Query Match 4.7%; Score 42; DB 4; Length 740;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 857 GGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 898
|||||
DB 689 GGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 730

RESULT 8
US-08-975-316-58

Sequence 38, Application US/08975316
Patent No. 5952486

GENERAL INFORMATION:
APPLICANT: BLOKSBERG, Leonard N., HAVUKKALA, Ilkka
APPLICANT: and GRIERSON, Alastair W.
TITLE OF INVENTION: MATERIALS AND METHODS FOR
TITLE OF INVENTION: THE MODIFICATION OF PLANT LIGNIN CONTENT
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESSES:


```

Query Match      4.7%; Score 42; DB 4; Length 1315;
Best Local Similarity 100.0%; Pred. No. 1e-07;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 857 GGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 898
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DB 1260 GGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1301

```

US-08-655-352-10
; Sequence 10, Application US/08655352
; Patent No. 6077991
; GENERAL INFORMATION:
; APPLICANT: Bachettira W. Poovaiiah, Zhinua Liu,
; APPLICANT: Shameekumar Patil, Daisuke Takezawa
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: PRODUCTION OF MALE-STERILE PLANTS
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klarquist Sparkman Campbell Leigh &
; ADDRESSEE: Whinston, LLP
; STREET: One World Trade Center
; STREET: 121 S.W. Salmon Street
; STREET: Suite 1600
; CITY: Portland
; STATE: Oregon
; COUNTRY: United States of America
; ZIP: 97204
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Disk, 3-1/2 inch
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/655,352
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/323,449
; FILING DATE: October 14, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Dow, Alan. E.
; REGISTRATION NUMBER: 35,123
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (503) 226-7391
; TELEFAX: (503) 228-9446
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1776 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double stranded
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; DESCRIPTION: Tobacco CcAMK cDNA and deduced amino-acid
; DESCRIPTION: sequence
; FEATURE:
; NAME/KEY: protein-coding sequence (not including
; NAME/KEY: stop codon)
; LOCATION: nucleotides 20-1570
US-08-655-352-10
Query Match 4.7%; Score 42; DB 3; Length 1776;
Best Local Similarity 100.0%; Pred. No. 9.7e-08;
Matches 42; Conservative 0; Indels 0; Gaps 0;
OY 857 GGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 898
Db 1719 GGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1760
RESULT 13
US-09-258-016-10
; Sequence 10, Application US/09258016
; Patent No. 6362395
; GENERAL INFORMATION:
; APPLICANT: Bachettira W. Poovaiiah, Zhinua Liu,
; APPLICANT: Shameekumar Patil, Daisuke Takezawa
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: PRODUCTION OF MALE-STERILE PLANTS
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:

ADDRESSEE: Klarquist Sparkman Campbell Leigh &
ADDRESSEE: Whinston, LLP
STREET: One World Trade Center
STREET: 121 S.W. Salmon Street
STREET: Suite 1600
CITY: Portland
STATE: Oregon
COUNTRY: United States of America
ZIP: 97204
COMPUTER READABLE FORM:
MEDIUM TYPE: Disk, 3-1/2 inch
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/258,016
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Stephens Jr., Donald L.
REGISTRATION NUMBER: 34,022
REFERENCE/DOCKET NUMBER: 4630-51994
TELECOMMUNICATION INFORMATION:
TELEPHONE: (503) 226-7391
TELEFAX: (503) 228-9446
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 1776 base pairs
TYPE: nucleic acid
STRANDEDNESS: double stranded
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
DESCRIPTION: Tobacco CcAMK cDNA and deduced amino-acid
DESCRIPTION: sequence
FEATURE:
NAME/KEY: protein-coding sequence (not including
NAME/KEY: stop codon)
LOCATION: nucleotides 20-1570
US-09-258-016-10
Query Match 4.7%; Score 42; DB 4; Length 1776;
Best Local Similarity 100.0%; Pred. No. 9.7e-08;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 857 GGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 898
Db 1719 GGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1760
RESULT 14
US-09-257-825B-10
; Sequence 10, Application US/09257825B
; Patent No. 6403352
; GENERAL INFORMATION:
; APPLICANT: Poovaiiah, Bachettira W.
; APPLICANT: Patil, Shameekumar
; APPLICANT: Takezawa, Daisuke
; TITLE OF INVENTION: Compositions and Methods for Production of Male-Sterile Plants
; FILE REFERENCE: 4630-51993
; CURRENT APPLICATION NUMBER: US/09/257,825B
; PRIOR FILING DATE: 1999-02-25
; PRIOR APPLICATION NUMBER: US 08/655,352
; PRIOR FILING DATE: 1996-05-23
; PRIOR APPLICATION NUMBER: US 60/014,743
; PRIOR FILING DATE: 1996-03-28
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 1776
; TYPE: DNA
; ORGANISM: Nicotiana tabacum
US-09-257-825B-10

Query Match 4.7%; Score 42; DB 4; Length 1776;
Best Local Similarity 100.0%; Pred. No. 9.7e-08;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 857 GGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 898
|||||
DB 1719 GGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1760

RESULT 15
US-08-606-505B-1
; Sequence 1, Application US/08606505B
; Patent No. 6114601
; GENERAL INFORMATION:
; APPLICANT: KIKUCHI, Yasuhiro
; APPLICANT: KIYOKAWA, Shigeto
; APPLICANT: SHIMADA, Yukinisa
; APPLICANT: OHBAYASHI, Masaya
; APPLICANT: SHIMADA, Ritsuko
; APPLICANT: OKINAKA, Yasushi
; TITLE OF INVENTION: NOVEL PLANT GENES
; NUMBER OF SEQUENCES: 67
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FITZPATRICK, CELLA, HARPER & SCINTO
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10112-3801
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette - 3.50 inch, 720 Kb storage.
; COMPUTER: IBM PS/4
; OPERATING SYSTEM: MS-DOS Ver3.30
; SOFTWARE: PATENT AID Ver1.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/606,505B
; FILING DATE: 23-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JPA4963/92
; FILING DATE: 02-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Peery, Lawrence S.
; REGISTRATION NUMBER: 31865
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-218-2100
; TELEFAX: 212-218-2200
; INFORMATION FOR SEQ ID NO: 1 :
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1824 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; ORIGINAL SOURCE:
; ORGANISM: Petunia hybrida
; STRAIN: Falcon Blue
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 116 to 1633
; IDENTIFICATION METHOD: by experiment
; US-08-606-505B-1

Query Match 4.7%; Score 42; DB 3; Length 1824;
Best Local Similarity 100.0%; Pred. No. 9.6e-08;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 856 GGCTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 897
|||||
DB 1783 GGCTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1824

Search completed: February 22, 2003, 06:08:15
Job time : 82.4172 secs

GenCore version 5.1.4_p5_4578
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OM nucleic - nucleic search, using sw model

Run on: February 22, 2003, 04:05:06 ; Search time 1445.72 Seconds
(without alignments)
10059.722 Million cell updates/sec

Title: US-09-832-320-1

Perfect score: 898
Sequence: 1 ctgcacgcactcgcacgtc.....aaaaaaaaaaaaaaaaaaaaa 898

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 16154066 seqs, 809774376 residues

Word size : 25

Total number of hits satisfying chosen parameters: 239749

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

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2: em_esthum:*
3: em_estln:*
4: em_estnu:*
5: em_estov:*
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8: em_hlc:*
9: gb_estl:*
10: gb_est2:*
11: gb_hlc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
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27: em_gss_rtd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	84	9.4	297	10	AM923743 DGI_59_A0
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5	48	5.3	1243	10	BE420593 HMM000.E0
6	45	5.0	145	14	BQ234664 hd48d10.g

c	7	45	5.0	178	9	A1452556
c	8	45	5.0	180	10	BE429386
c	9	45	5.0	192	12	BG122481
c	10	45	5.0	229	10	AM169684
c	11	45	5.0	300	13	BT002437
c	12	45	5.0	309	9	A1378624
c	13	45	5.0	340	9	A1357509
c	14	45	5.0	355	10	AM151031
c	15	45	5.0	457	10	AM264516
c	16	45	5.0	540	9	A1366748
c	17	45	5.0	953	13	BI159439
c	18	45	5.0	1068	14	BM608835
c	19	44	4.9	255	9	A1624157
c	20	44	4.9	354	12	BG403840
c	21	44	4.9	364	10	BE051700
c	22	44	4.9	383	9	A1656882
c	23	44	4.9	403	14	BQ396010
c	24	44	4.9	425	13	BI496218
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c	28	43	4.8	90	13	BI494772
c	29	43	4.8	97	13	BI783370
c	30	43	4.8	100	9	A1336823
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c	35	43	4.8	120	10	AM747569
c	36	43	4.8	131	14	BM966206
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c	43	43	4.8	171	13	BG381493
c	44	43	4.8	174	14	BQ089993
c	45	43	4.8	177	9	AA983883

ALIGNMENTS

RESULT 1
LOCUS BE512404 486 bp mRNA linear EST 07-AUG-2000
DEFINITION 946070F05.y1 946 - tassal primordium prepared by Schmidt lab zea
ACCESSION BE512404
VERSION BE512404.1 GI:9733652
KEYWORDS
SOURCE
ORGANISM

REFERENCE

1 (bases 1 to 486)
Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade: Panicoidae; Andropogoneae; Zea.
Zea mays.
Zea mays.
Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade: Panicoidae; Andropogoneae; Zea.

JOURNAL

Unpublished (1999)
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 8227
Fax: 650 723 8221
Email: walbot@stanford.edu
Plate: 946070 row: F column: 05.
location/Qualifiers
1. 486
/organism="Zea mays"

FEATURES

source

```

/cultivar="OH43"
/db_xref="taxon:4577"
/clone_lib="946 - tassell primordium prepared by Schmidt
lab"
/tissue_type="tassels"
/dev_stage="just after the transition from vegetative to
inflorescence development"
/lab_host="XLOLR"
/notes="Organ: tassels; Vector: HybriZAP; Site.1: EORI;
Site.2: XhoI; George Chuck dissected immature tassels
between 1mm and 3mm. Sharon Stanfield prepared the cDNA
library in HybriZAP. Sample insert size range was 350 bp
to 3 kb with a 1 kb average."

BASE COUNT      100 a      131 c      150 g      105 t
ORIGIN

Query Match      29.4%; Score 264; DB 10; Length 486;
Best Local Similarity 100.0%; Pred. No. 3e-51;
Matches 264; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 600 TGGCCACGCGGCGCCACGCTCAGCTGCTGCTGTACACCCGCGCAGCGCAGCGGC 659
    |||||||
Db 177 TGGCGCCACGCGGCGCCACGCTCAGCTGCTGCTGTACACCCGCGCAGCGGC 236
    |||||||

QY 660 CAGAGCCCCCTACAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCT 719
    |||||||
Db 237 CAGAGCCCCCTACAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCT 296
    |||||||

QY 720 GCGCGCGCGCAGCGGAGTACAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCT 779
    |||||||
Db 297 GCGCGCGCGCAGCGGAGTACAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCT 356
    |||||||

QY 780 GTTTTGTGTGTATATCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 839
    |||||||
Db 357 GTTTTGTGTGTATATCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 416
    |||||||

QY 840 ATCAGCTTTTGTGCGCGGTAAAA 863
    |||||||
Db 417 ATCAGCTTTTGTGCGCGGTAAAA 440
    |||||||

RESULT 2
AM923743      297 bp      mRNA      linear      EST 19-JUL-2000
LOCUS
DEFINITION   Dcl_59_A04.g1_A002 Dark Grown 1 (Dcl) Sorghum bicolor cDNA, mRNA
ACCESSION    AM923743
VERSION      AM923743.1 GI:8089568
KEYWORDS     EST.
SOURCE       sorghum.
ORGANISM     sorghum bicolor
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Sorghum.
1 (bases 1 to 297)
Cordonnier-Pratt,M.-M., Gingle,A., Marsala,C., Sudman,M. and Pratt
,L.H.
An EST database from Sorghum: dark-grown seedlings
Unpublished (2000)
Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
Email: mmp@prattuga.edu
Sequences have been trimmed to exclude PolyA, vector and regions
below Phred quality 16. The threshold for highest quality sequence
is 20.
Seq primer: PolYTmix
High quality sequence start: 16
High quality sequence stop: 289
POLYA-No.

```

```

FEATURES
source
Location/Qualifiers
1..297
/organism="Sorghum bicolor"
/db_xref="taxon:4558"
/clone_lib="Dark Grown 1 (Dcl)"
/notes="Organ: 5-day-old dark-grown seedlings; Vector:
lambda zap; Site.1: XhoI; Site.2: EORI; The library was
made from poly-A RNA in the cloning vector lambda zap II.
Clones to be sequenced were prepared by mass excision."

BASE COUNT      46 a      86 c      97 g      67 t      1 others
ORIGIN

Query Match      9.4%; Score 84; DB 10; Length 297;
Best Local Similarity 100.0%; Pred. No. 3.1e-10;
Matches 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 597 AGCTGCGCCACGCGGCGCCACGCTCAGCTGCTGCTGTACACCCGCGCAGCGTGCAG 656
    |||||||
Db 43 AGCTGCGCCACGCGGCGCCACGCTCAGCTGCTGCTGTACACCCGCGCAGCGTGCAG 102
    |||||||

QY 657 GCGCAGAGCCCCCTACTAGCTAGCT 680
    |||||||
Db 103 GCGCAGAGCCCCCTACTAGCTAGCT 126
    |||||||

RESULT 3
BM101325      362 bp      mRNA      linear      EST 23-JUL-2002
LOCUS
DEFINITION   Ebp101_S0003_113_R pistill, 1 DPA, no treatment, cv Optic, Ebp101
Hordenum vulgare cDNA clone Ebp101_S0003_113 5', mRNA sequence.
ACCESSION    BM101325
VERSION      BM101325.2 GI:21944137
KEYWORDS     EST.
SOURCE       Hordenum vulgare.
ORGANISM     Hordenum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
; Triticeae; Hordenum.
1 (bases 1 to 362)
Hedley,P., Liu,H., Caldwell,D., McCallum,N., Mudie,S., Cardle,L.,
Ramsay,L., Machray,G., Marshall,D.F.M. and Waugh,R.
Development of Barley Transcriptome Resources
Unpublished (2001)
On Nov 21, 2001 this sequence version replaced gi:17032393.
Contact: Waugh R, Marshall DF
Genome Dynamics/Computational Biology
Scottish Crop Research Institute
Invergowrie, Dundee, DD2 5DA, Scotland, UK
Tel: 00 44 1382 562731
Fax: 00 44 1382 562426
Email: estescrl.sari.ac.uk
All sequence has a Phred quality score of 20 or over
Seq primer: M13 reverse.
Location/Qualifiers
1..362
/organism="Hordenum vulgare"
/cultivar="Optic"
/db_xref="taxon:4513"
/clone="Ebp101_S0003_113"
/clone_lib="pistill, 1 DPA, no treatment, cv Optic, Ebp101"
/tissue_type="pistill"
/dev_stage="1 DPA"
/lab_host="DH10B"
/notes="Vector: pSPORT1; Site.1: Sal I; Site.2: Not I;
Non-normalised library, directionally cloned into pSPORT1.
Derived from pistils dissected from developing grains (24
hours post anthesis) in glasshouse grown barley plants.
Developed as part of the barley transcriptome resources of
BBSRC/SEERAD funded cereal IGF (Investigating Gene
Function) project."

BASE COUNT      57 a      139 c      129 g      37 t
ORIGIN

```

Query Match 5.6%; Score 50; DB 13; Length 362;
 Best Local Similarity 100.0%; Pred. No. 0.013;
 Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 408 GCCAGCCCTACGGCGGCGAACCAGGCGGTGGCGAGCTACCGCGCGCC 457
 |||||||
 DB 98 GCCAGCCCTACGGCGGCGAACCAGGCGGTGGCGAGCTACCGCGCGCC 147

RESULT 4
 BG343299 996 bp mRNA linear EST 22-OCT-2001
 LOCUS HVSMEG0005F16f Hordeum vulgare pre-anthesis spike EST library
 DEFINITION HVCNDA0008 (white to yellow anther) Hordeum vulgare cDNA clone
 HVSMEG0005F16f, mRNA sequence.
 BG343299
 ACCESSION BG343299.1 GI:13155628
 VERSION EST.
 KEYWORDS Hordeum vulgare.
 SOURCE Hordeum vulgare.
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
 ; Triticeae; Hordeum.
 1 (bases 1 to 996)
 Wing, R., Close, T.J., Kleinhofs, A., Wise, R., Begum, D., Frisch, D., Yu
 , Y., Henry, D., Palmer, M., Rambo, T., Simmons, J., Choi, D.W., Fenton
 , R.D., Close, S.J., Oates, R., and Main, D.
 Development of a genetically and physically anchored EST resource
 for barley genomics: Morex pre-anthesis spike cDNA library
 Unpublished (2001)
 CONTACT: Wing RA
 JOURNAL Clemson University Genomics Institute
 COMMENT 100 Jordan Hall, Clemson, SC 29634, USA
 Tel: 864 656 7288
 Fax: 864 656 4293
 Email: rwing@clemson.edu
 Total bp bases = 471
 Seq primer: AATTACCTCCTACCTAAAGG
 High quality sequence stop: 717.
 Location/Qualifiers
 1..996
 /organism="Hordeum vulgare"
 /cultivar="Morex"
 /db_xref="taxon:4513"
 /clone="HVSMEG0005F16f"
 /clone_lib="Hordeum vulgare pre-anthesis spike EST library
 HVCNDA0008 (white to yellow anther)"
 /tissue_type="pre-anthesis spike"
 /lab_host="SOLR"
 /note="Vector: lambdaZAP; Site 1: EcoRI; Site 2: XhoI;
 Plants were grown in the greenhouse at the University of
 California, Riverside (Fenton, SJ Close, TJ Close). Whole
 spike with awns trimmed were collected at white, green and
 yellow anther stages (Fenton). Total RNA was prepared from
 each pool, equal quantities of all three RNA pools were
 combined, poly(A) RNA was purified from the mixture, one
 primary unamplified cDNA library was made, and 1 million
 pfu were in vivo excised to give Bluescript SK(-) cDNA
 phagemids. These steps were performed in the TJ Close lab
 (Choi) at the University of California, Riverside.
 Phagemids were plated and picked at the Clemson University
 Genomics Institute (CUGI) (Begum, Palmer, Frisch, Atkins
 and Wing) Plasmid DNA preparations, DNA sequencing and
 sequence analysis were performed at CUGI (Wing, Yu, Frisch
 , Henry, Simmons, Oates, Rambo, Main). The sequence has
 been trimmed to remove vector sequence and contains a
 minimum of 100 bases of phred value 20 or above. For more
 details on library preparation and sequence analysis see
 http://www.genome.clemson.edu/projects/barley. To order
 this clone see http://www.genome.clemson.edu/orders Also
 see Close TJ, Wing R, Kleinhofs A, Wise R (2001)
 Genetically and physically anchored EST resources for

barley genomics. Barley Genetics Newsletter 31:29-30.
 (http://wheat.pw.usda.gov/gnpages/ymr/31/cover.html)."

BASE COUNT 183 a 310 c 377 g 123 t 3 others

Query Match 5.6%; Score 50; DB 12; Length 996;
 Best Local Similarity 100.0%; Pred. No. 0.0049;
 Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 408 GCCAGCCCTACGGCGGCGAACCAGGCGGTGGCGAGCTACCGCGCGCC 457
 |||||||
 DB 399 GCCAGCCCTACGGCGGCGAACCAGGCGGTGGCGAGCTACCGCGCGCC 448

RESULT 5
 BE420593 1243 bp mRNA linear EST 24-JUL-2000
 LOCUS HNM000.E06 ITEC HMM Barley leaf library Hordeum vulgare cDNA clone
 DEFINITION HNM000.E06, mRNA sequence.
 BE420593
 ACCESSION BE420593.1 GI:9418436
 VERSION EST.
 KEYWORDS Hordeum vulgare.
 SOURCE Hordeum vulgare.
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
 ; Triticeae; Hordeum.
 1 (bases 1 to 1243)
 Anderson, O.A., Appels, R., Bailey, P., Blake, J., Close, T., Cloutier
 , S., Dubcovsky, J., Feuillet, C., Gale, M., Graner, A., Gustafson, P.,
 Herrmann, R.G., Holton, T., Jacquemin, J.M., Jia, J., Joudrier, P.,
 Langridge, P., Izzo, G.R., Lin, J.J., McGuire, P., Ogilvie, Y.,
 Pecchioni, N., Qualset, C., Schuch, W., Selvaraj, G., Shariflou, M.,
 Sorrells, M., Warburton, M. and Wenzel, G.
 International Triticeae EST Cooperative (ITEC): Production of
 Expressed Sequence Tags for Species of the Triticeae
 Unpublished (2000)
 JOURNAL Contact: Herrmann RG
 COMMENT Botanisches Institut der LMU
 Menzinger Str. 67, D-80638 Munchen GERMANY
 Fax: 49 30 171683
 Email: herrmann@botanik.biologie.uni-muenchen.de
 International Triticeae EST Cooperative (ITEC)
 http://wheat.pw.usda.gov/genome.
 Location/Qualifiers
 1..1243
 /organism="Hordeum vulgare"
 /cultivar="Barke"
 /db_xref="taxon:4513"
 /clone="HNM000.E06"
 /clone_lib="ITEC HMM Barley leaf library"
 /tissue_type="leaf"
 /dev_stage="14 day old"
 /note="Vector: pBluescriptSK(-); 850 bp average insert
 size."

BASE COUNT 282 a 269 c 364 g 274 t 54 others

Query Match 5.3%; Score 48; DB 10; Length 1243;
 Best Local Similarity 100.0%; Pred. No. 0.011;
 Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 851 TTGCGCGGTAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAG 898
 |||||||
 DB 615 TTGCGCGGTAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAG 662

RESULT 6
 BQ234664 145 bp mRNA linear EST 03-MAY-2002
 LOCUS hd48d10.g1 Canis Total Brain cDNAs Canis familiaris cDNA clone
 DEFINITION hd48d10 5', mRNA sequence.
 ACCESSION BQ234664

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VERSION      BQ234664.1  GI:20430537
KEYWORDS     EST.
SOURCE       dog.
ORGANISM     Canis familiaris
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE    1 (bases 1 to 145)
AUTHORS      O'Shaughnessy,A.L., Palmer,L., McCombie,W.R., Baker,J.P., Bahret,A.,
             Cannals,D., Dedhia,N.N., de la Bastide,M., Katzenberger,F., King
             L., Kirchoff,K.A., Miller,B., Muller,S., Nascimento,L.U., Preston
             R.R., Shah,R.S., Spiegel,L.A., Zutavern,T., Santos,L. and Hannon
             G.J.
TITLE        Expressed sequence tags from Canis familiaris (dog) (5_2002)
JOURNAL      Unpublished (2002)
COMMENT      Contact: W. Richard McCombie
             Lita Annenberg Hazen Genome Sequencing Center
             Cold Spring Harbor Laboratory
             PO Box 100, Cold Spring Harbor, NY 11724, USA
             Tel: 516 367 8884
             Fax: 516 367 8874
             Email: mccombie@cshl.org
             Plate: hd48 row: d column: 10
             Seq primer: -21M13univrev
             High quality sequence stop: 145.
FEATURES     location/Qualifiers
             1..145
             /organism="Canis familiaris"
             /db_xref="taxon:9615"
             /clone_id="Canis.Total.Brain.CDNAs"
             /note="Vector: Lambda Zap II; The library was provided by
             Greg Hannon and Lee Santos (Cold Spring Harbor Laboratory
             ). This library is oligo(dT) primed using stratagene zap
             cDNA synthesis kit. It was made from dog whole brain
             cells. Please contact Greg Hannon (hannon@cshl.org) with
             any library related inquiries."
BASE COUNT   14 a 14 c 19 g 98 t
ORIGIN
Query Match 5.0%; Score 45; DB 14; Length 145;
Best Local Similarity 100.0%; Pred. No. 0.42;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 854 CCGGGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 898
Db 109 CCGGGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 65
RESULT 7
LOCUS       A1452556 178 bp mRNA linear EST 13-APR-1999
DEFINITION tJ22a03.x1 NCI-CGAP Gas4 Homo sapiens cDNA clone IMAGE:2142220 3'
             similar to contains element OFR repetitive element; mRNA
             sequence.
ACCESSION   A1452556
VERSION     A1452556
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE    1 (bases 1 to 178)
AUTHORS      NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
             National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
             Tumor Gene Index
             Unpublished (1997)
COMMENT      Contact: Robert Strausberg, Ph.D.
             Email: cga@bbs-femail.nih.gov
             Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
             Emert-Buck, M.D., Ph.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center

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Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
www-bio.lnl.gov/bbrp/image/image.html
Insert Length: 764 Std Error: 0.00
Seq primer: -40UP from Gldco
High quality sequence stop: 166.
FEATURES     Location/Qualifiers
             source
             1..178
             /organism="Homo sapiens"
             /db_xref="taxon:9606"
             /clone_image="2142220"
             /clone_id="NCI-CGAP.Gas4"
             /tissue_type="poorly differentiated adenocarcinoma with
             signet ring cell features"
             /lab_host="DH10B"
             /note="Organ: stomach; Vector: pCMV-SPORT6; Site: 1; Salt;
             Site: 2; NotI; Cloned unidirectionally. Primer: Oligo dT.
             Average insert size 1.65 kb. Life Technologies catalog #:
             11549-011"
BASE COUNT   34 a 40 c 16 g 88 t
ORIGIN
Query Match 5.0%; Score 45; DB 9; Length 178;
Best Local Similarity 100.0%; Pred. No. 0.35;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 854 CCGGGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 898
Db 70 CCGGGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 26
RESULT 8
LOCUS       BE429386 180 bp mRNA linear EST 26-JUL-2000
DEFINITION MTD017.E07F990621 TTEC MTD durum wheat Root Library Triticum
             turgidum subsp. durum cDNA clone MTD017.E07, mRNA sequence.
ACCESSION   BE429386
VERSION     BE429386
KEYWORDS    EST.
SOURCE      durum wheat.
ORGANISM    Triticum turgidum subsp. durum
             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
             Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poaceae
             ; Triticaceae; Triticum.
REFERENCE    1 (bases 1 to 180)
AUTHORS      Anderson,O.A., Appels,R., Bailey,P., Blake,T., Close,T., Cloutier
             S., Dubcovsky,J., Feuillet,C., Gale,M., Graner,A., Gustafson,P.,
             Herrmann,R.G., Holton,T., Jacquemlin,J.M., Jia,J., Joudrier,P.,
             Langridge,P., Lazo,G.R., Lin,J.J., McGuire,P., Ogihara,Y.,
             Sorrells,M., Wardlaw,I.M., and Wenzel,G.
             International Triticaceae EST Cooperative (TTEC): Production of
             Expressed Sequence Tags for Species of the Triticaceae
             Unpublished (2000)
COMMENT      Contact: Joudrier P
             INRA, Unite de Biochimie et Biologie Moleculaire des Cereales
             2, place VIALA, 34060 Montpellier cedex 01 FRANCE
             Tel: 33 4 99 61 23 84
             Fax: 33 4 99 61 23 48
             Email: joudrier@enscm.inra.fr
             International Triticaceae EST Cooperative (TTEC)
             http://wheat.pw.usda.gov/genome.
FEATURES     Location/Qualifiers
             source
             1..180
             /organism="Triticum turgidum subsp. durum"
             /cultivar="Silihana"
             /db_xref="taxon:4567"
             /clone_image="MTD017.E07"
             /clone_id="TTEC.MTD.Durum.Wheat.Root.Library"
             /tissue_type="root"
             /note="stage="3-day-old seedling, water-stressed"
             /note="vector: pSPORT1; T7 primers used. See pSPORT1
             polylinker site. 0.3-2.0 kbp average insert size."

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BASE COUNT      61 a      20 c      63 g      14 t      22 others
ORIGIN
Query Match      5.0%; Score 45; DB 10; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.34;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      854 CCGGGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 898
Db      1 CCGGGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 45

RESULT 9
Bg122481      192 bp      mRNA      linear      EST 30-JAN-2001
LOCUS      602353281F1 NIH_MGC_90 Homo sapiens cDNA clone IMAGE:4451253 5',
DEFINITION      mRNA sequence.
ACCESSION      Bg122481
VERSION      Bg122481.1 GI:12615990
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 192)
REFERENCE      NIH-MGC http://mgi.nci.nih.gov/.
AUTHORS      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL      Unpublished (1999)
COMMENT      Contact: Robert Strausberg, Ph.D.
              Email: cgabs-remail.nih.gov
              Tissue Procurement: ATCC
              cDNA Library Preparation: Life Technologies, Inc.
              DNA Sequencing by: Incyte Genomics, Inc.
              Clone distribution: MGC clone distribution information can be
              found through the I.M.A.G.E. Consortium/LLNL at:
              http://image.llnl.gov
              Plate: LAM10238 row: b column: 22
              High quality sequence stop: 145.
              Location/Qualifiers
                1. 192
                  /organism="Homo sapiens"
                  /db_xref="taxon:9606"
                  /clone="IMAGE:4451253"
                  /clone_lib="NIH_MGC_90"
                  /tissue_type="adenocarcinoma, cell line"
                  /lab_host="DH10B (phage-resistant)"
                  /note="Organ: liver; Vector: pCMV-SPORT6; Site_1: NotI;
                  Site_2: SalI; Cloned unidirectionally; Oligo-dt primed.
                  Average insert size 1.7 kb. Library enriched for
                  full-length clones and constructed by Life Technologies.
                  Note: this is a NIH_MGC library."

BASE COUNT      143 a      8 c      22 g      19 t
ORIGIN
Query Match      5.0%; Score 45; DB 12; Length 192;
Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      854 CCGGGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 988
Db      52 CCGGGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 96

RESULT 10
AM169684      229 bp      mRNA      linear      EST 12-NOV-1999
LOCUS      x130107.x1 NCI_CGAP_Ut2 Homo sapiens cDNA clone IMAGE:2658781 3',
DEFINITION      mRNA sequence.
ACCESSION      AM169684
VERSION      AM169684.1 GI:6401209
KEYWORDS      EST.
SOURCE      human.

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ORIGIN      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 229)
REFERENCE      NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS      National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
              Tumor Gene Index
              Unpublished (1997)
JOURNAL      Contact: Robert Strausberg, Ph.D.
COMMENT      Email: cgabs-remail.nih.gov
              Tissue Procurement: Christopher Moskalko, M.D., Ph.D., Michael R.
              Emerit-Buck, M.D., Ph.D.
              cDNA Library Preparation: Life Technologies, Inc.
              CDNA Library Arrayed by: Greg Lennon, Ph.D.
              DNA Sequencing by: Washington University Genome Sequencing Center
              Clone distribution: NCI-CGAP clone distribution information can be
              found through the I.M.A.G.E. Consortium/LLNL at:
              www-bio.llnl.gov/bbrp/image/image.html

FEATURES
source
1. 229
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2658781"
/clone_lib="NCI_CGAP_Ut2"
/tissue_type="moderately-differentiated endometrial
adenocarcinoma, 3 pooled tumors"
/lab_host="DH10B"
/note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.85 kb. Life Technologies catalog #:
11559-012"

BASE COUNT      55 a      46 c      40 g      88 t
ORIGIN
Query Match      5.0%; Score 45; DB 10; Length 229;
Best Local Similarity 100.0%; Pred. No. 0.27;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      854 CCGGGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 898
Db      59 CCGGGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 15

RESULT 11
BI002437      300 bp      mRNA      linear      EST 13-JUN-2001
LOCUS      MR3-HN0150-220101-007-h08 HN0150 Homo sapiens cDNA, mRNA sequence.
DEFINITION      MR3-HN0150-220101-007-h08 HN0150 Homo sapiens cDNA, mRNA sequence.
ACCESSION      BI002437
VERSION      BI002437.1 GI:14406511
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 300)
REFERENCE      Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
              Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
              Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H.,
              Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare
              M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
              Simpson, A.J.
              Shotgun sequencing of the human transcriptome with ORF expressed
              sequence tags
              Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
JOURNAL      Contact: Simpson A.J.G.
MEDLINE      Laboratory of Cancer Genetics
              Ludwig Institute for Cancer Research
              Rua Prof. Antonio Pudente 109, 4 andar, 01509-010, Sao Paulo-SP,
              COMMENT

```

Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?l=MR3&t=2-MR3-HN0150-220101-007-h08&t=3=2001-01-22&t=1)
Seq primer: puc 18 forward
High quality sequence stop: 276.

FEATURES

source

1..300
Location/Qualifiers

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_id="HN0150"
/dev_stage="Adult"

/note="Organ: head,normal; Vector: puc18; Site:1: SmaI; Site:2: SmaI; A mini-library was made by cloning products derived from ORESMPS PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
BASE COUNT 50 a 60 c 41 g 149 t
ORIGIN

Query Match 5.0%; Score 45; DB 13; Length 300;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 854 CCGGGTAAAAA
Db 284 CCGGGTAAAAA
LOCUS A1378624
DEFINITION A1378624
ACCESSION A1378624
VERSION A1378624
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 309)
NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Insert length: 1405 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 299.

FEATURES

source

1..309
Location/Qualifiers

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_id="IMAGE:2070196"
/clone_id="Soares_NHMPU_S1"
/tissue_type="Pooled human melanocyte, fetal heart, and
pregnant uterus"
/lab_host="DH10B"
/note="Organ: mixed (see below); Vector: pT73D-Pac
(Pharmacia) with a modified polylinker; Site:1: Not I;
Site:2: Eco RI; Equal amounts of plasmid DNA from three
normalized libraries (melanocyte 2NDHM, pregnant uterus
NBHPU, and fetal heart NBH19M) were mixed, and ss circles

were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 260232-265223, 340488-345479, and 484488-489479."

BASE COUNT

73 a 58 c 78 g 100 t

Query Match 5.0%; Score 45; DB 9; Length 309;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 854 CCGGGTAAAAA
Db 54 CCGGGTAAAAA
LOCUS A1537509
DEFINITION A1537509
ACCESSION A1537509
VERSION A1537509
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 340)
NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CCAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
www.bio.lnl.gov/dbp/image/image.html
Insert length: 929 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 329
POLY-A-NO.

FEATURES

Location/Qualifiers

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_id="IMAGE:2187329"
/clone_id="NCI CGAP Gas4"
/tissue_type="Poorly differentiated adenocarcinoma with
signet ring cell features"
/lab_host="DH10B"
/note="Organ: stomach; Vector: pCMV-SPORT6; Site:1: SalI;
Site:2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.69 kb. Life Technologies catalog #:
11549-011"

BASE COUNT

63 a 74 c 95 g 108 t

Query Match 5.0%; Score 45; DB 9; Length 340;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 854 CCGGGTAAAAA
Db 101 CCGGGTAAAAA
LOCUS A1537509
DEFINITION A1537509
ACCESSION A1537509
VERSION A1537509
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 340)
NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CCAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
www.bio.lnl.gov/dbp/image/image.html
Insert length: 929 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 329
POLY-A-NO.

RESULT 14
 AM151031/C
 LOCUS xq43q09.x1 NCI_CGAP_Utl Homo sapiens cDNA clone IMAGE:2630368 3',
 DEFINITION mRNA sequence.
 ACCESSION AM151031
 VERSION AM151031.1 GI:6198929
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 355)
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: cgaps-remail.nih.gov
 Tissue Procurement: Christopher Moskalkuk, M.D., Ph.D., Michael R.
 Emmert-Buck, M.D., Ph.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
 Seq primer: -400P from Glibco
 High quality sequence stop: 345.
 Location/Qualifiers
 1..355
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:2630368"
 /clone_lib="NCI_CGAP_Utl"
 /tissue_type="well-differentiated endometrial
 adenocarcinoma, 7 pooled tumors"
 /lab_host="DH10B"
 /note="Organ: uterus; Vector: PCMV-SPORT6; Site:1; SalI;
 Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt.
 Average insert size 1.75 kb. Life Technologies catalog #: 11538-014"
 11538-014"
 BASE COUNT 88 a 64 c 100 g 102 t 1 others
 ORIGIN
 Query Match 5.0%; Score 45; DB 10; Length 355;
 Best Local Similarity 100.0%; Pred. No. 0.18;
 Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 854 CCGGGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 898
 ||||||||||||||||||||||||||||||||||||||||||||
 Db 58 CCGGGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 14
 RESULT 15
 AM264516/C
 LOCUS xrl0e06.x1 NCI_CGAP_Brn53 Homo sapiens cDNA clone IMAGE:2759170 3',
 DEFINITION similar to SW:PF12_PIG P51525 PROPHENIN-2 PRECURSOR; contains
 element MSRI repetitive element; mRNA sequence.
 ACCESSION AM264516
 VERSION AM264516.1 GI:6641332
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 457)
 NCI/NINDS-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 National Cancer Institute / National Institute of Neurological
 Disorders and Stroke, Brain Tumor Genome Anatomy Project

JOURNAL
 COMMENT
 (CGAP/BRGAP), Tumor Gene Index
 Unpublished (1998)
 Contact: Robert Strausberg, Ph.D.
 Email: cgaps-remail.nih.gov
 Tissue Procurement: Chris Moskalkuk, M.D., Ph.D., Michael R.
 Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life
 Technologies, Inc. cDNA Library Arrayed by: Christa Prange, The
 I.M.A.G.E. Consortium DNA Sequencing by: Washington University
 Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
 Possible reversed clone: polyT not found
 Seq primer: -400P from Glibco
 High quality sequence stop: 375.
 Location/Qualifiers
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 /db_xref="taxon:9606"
 /clone="IMAGE:2759170"
 /clone_lib="NCI_CGAP_Brn53"
 /tissue_type="three pooled meningiomas"
 /lab_host="DH10B"
 /note="Organ: brain; Vector: PCMV-SPORT6; Site:1; SalI;
 Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt.
 Library constructed by Life Technologies."
 BASE COUNT 98 a 117 c 107 g 135 t
 ORIGIN
 Query Match 5.0%; Score 45; DB 10; Length 457;
 Best Local Similarity 100.0%; Pred. No. 0.14;
 Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 854 CCGGGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 898
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 Db 98 CCGGGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 54
 Search completed: February 22, 2003, 06:06:21
 job time : 1474.72 secs

100

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 22, 2003, 03:42:31 ; Search time 2492.4 Seconds

(without alignments)
10485.621 Million cell updates/sec

Title: US-09-832-320-1

Perfect score: 898
Sequence: 1 clcgacgcactgcgcgcgc.....aaaaaaaaaaaaaaaaaaaaa 898

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 2054640 seqs, 14551402878 residues

Word size : 25

Total number of hits satisfying chosen parameters: 128069

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

GenEmbl:*
1: gb_da:*
2: gb_hcg:*
3: gb_in:*
4: gb_in:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_ph:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_da:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_ov:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vl:*
30: em_hcg_hum:*
31: em_hcg_inv:*
32: em_hcg_other:*
33: em_hcg_mus:*
34: em_hcg_pln:*
35: em_hcg_rtd:*
36: em_hcg_mam:*
37: em_hcg_vrt:*
38: em_sy:*
39: em_hcg_hum:*
40: em_hcg_mus:*
41: em_hcg_other:*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	45	5.0	2445	9 BC019562	BC019562 Homo sapi
2	44	4.9	1981	3 AY070835	AY070835 Drosophila
3	43	4.8	293	6 AX187087	AX187087 Sequence
4	43	4.8	1032	8 AF043538	AF043538 Arabidops
5	43	4.8	1091	6 AX053122	AX053122 Sequence
6	43	4.8	1303	10 BC004060	BC004060 Mus muscu
7	43	4.8	1445	9 HSM802527	HSM802527 Homo sapi
8	43	4.8	1463	10 BC005424	BC005424 Mus muscu
9	43	4.8	1835	6 AR202048	AR202048 Sequence
10	43	4.8	1853	9 HSU58996	HSU58996 Homo sapien
11	43	4.8	1913	10 BC003999	BC003999 Mus muscu
12	43	4.8	2668	3 SSA283335	SSA283335
13	43	4.8	3280	5 AF069757	AF069757 Salmo sal
14	43	4.8	3415	10 AF361078	AF361078 Mus muscu
15	43	4.8	5012	3 AY069824	AY069824 Drosophila
16	43	4.8	72652	8 NCB912	NCB912 Neurospor
17	43	4.8	74417	8 NCB1D4	NCB1D4 Neurospor
18	43	4.8	103308	9 AC092491	AC092491 Homo sapi
19	43	4.8	116856	2 AC098429	AC098429 Rattus no
20	43	4.8	142350	2 AC120122	AC120122 Mus muscu
21	43	4.8	159708	2 AC113651	AC113651 Rattus no
22	43	4.8	169037	2 AC101756	AC101756 Mus muscu
23	43	4.8	174541	2 AC106665	AC106665 Rattus no
24	43	4.8	175916	2 AC007747	AC007747 Homo sapi
25	43	4.8	178534	2 AC100726	AC100726 Mus muscu
26	43	4.8	178623	2 AC099704	AC099704 Mus muscu
27	43	4.8	179155	2 AC119541	AC119541 Rattus no
28	43	4.8	193521	2 AC115916	AC115916 Mus muscu
29	43	4.8	194905	9 AC068896	AC068896 Homo sapi
30	43	4.8	218856	2 AC099282	AC099282 Rattus no
31	43	4.8	221936	2 AC102019	AC102019 Mus muscu
32	43	4.8	222185	2 AC127697	AC127697 Mus muscu
33	43	4.8	224448	2 PFMA4P4	PFMA4P4 Plasmodiu
34	43	4.8	232452	2 AC099393	AC099393 Rattus no
35	43	4.8	256774	2 AC116964	AC116964 Dictyoste
36	42	4.7	447	9 AK026855	AK026855 Homo sapi
37	42	4.7	488	9 BC003678	BC003678 Homo sapi
38	42	4.7	518	8 OSJ592	OSJ592 Quercus s
39	42	4.7	595	6 AX090442	AX090442 Sequence
40	42	4.7	740	6 AR066486	AR066486 Sequence
41	42	4.7	740	6 AR074099	AR074099 Sequence
42	42	4.7	740	6 AR143611	AR143611 Sequence
43	42	4.7	740	6 BD005647	BD005647 Materials
44	42	4.7	741	6 AR074149	AR074149 Sequence
45	42	4.7	741	6 BD005697	BD005697 Materials

ALIGNMENTS

RESULT 1
LOCUS BC019562 2445 bp, mRNA linear PRI 22-JAN-2002
DEFINITION Homo sapiens, clone IMAGE:3451144, mRNA, partial cds.
ACCESSION BC019562
VERSION BC019562.1 GI:18042964
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2445)
AUTHORS Strausberg R
TITLE Direct Submision
JOURNAL Submitted (19-DEC-2001) National Institutes of Health, Mammalian

Prod. No. is the number of results predicted by chance to have a

REMARK
COMMENT

Gene Collection (MGC), Cancer Genomics office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 Contact: MGC help desk
 Email: cgabs-remail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: The I.M.A.G.E. Consortium (LNL)
 Sequencing Center
 Center code: BCM-HGSC
 Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
 Contact: amgdbcm.tmc.edu
 Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Hale, S.M., Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M., Richards, S., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://lml.lnl.gov>
 Series: IRAC Plate: 19 Row: c Column: 17.

FEATURES

source

Location/Qualifiers
 1..2445

CDS

/organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:3451144"
 /tissue_type="Placenta, choriocarcinoma"
 /clone_lib="NIH_MGC_10"
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 /note="Vector: pCMV-Sport6"
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 DYSVKIKFSGEDPKTKQPKQYKQYTYGRRLSSVSSMRSAKEVALQBEHKICLST
 VLELVKCPDAVAVPSPMSVSPFILLSTVTRCVQLRITMGAMNNILFLVSGD
 QKTVGLTSLFEGVQLCLTAPVIGYIMDWRLKECEDSEEPERKDNQGEKKRR
 DRQIKITNARAFATNLLVGFVTCIPNLPQILSPILATIVRGFISAVGGLY
 AAVPSTQFSLTGLTSLISALFALLOPFLAMGFLSGDPLVNVVGLLTLSTLGGC
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BASE COUNT
ORIGIN

Query Match 5.0%, Score 45; DB 9; Length 2445;
 Best Local Similarity 100.0%; Pred. No. 2.3e-11;
 Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 854 CCGGGTAAAAA
 Db 2319 CCGGGTAAAAA

RESULT 2
 LOCUS AY070835 1981 bp mRNA linear INV 20-DEC-2001
 DEFINITION Drosophila melanogaster GH06691 full length cDNA.
 ACCESSION AY070835
 VERSION AY070835.1 GI:17944780
 KEYWORDS FLI.CDNA.
 SOURCE Drosophila melanogaster.
 ORGANISM Drosophila melanogaster.
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 Ephydroidea; Drosophilidae; Drosophila.

REFERENCE
AUTHORS

Stephenson, M., Brokstein, P., Hong, L., Agbayani, A., Carlson, J.,
 Champagne, M., Chavez, C., Dorsett, V., Drenth, D., Farfan, D., Fritse, E.,
 George, R., Gonzalez, M., Guarin, H., Krommiller, B., Li, P., Liao, G.,
 Miranda, A., Mungall, C.J., Nuno, J., Pacle, J., Paragas, V., Park, S.,
 Patel, S., Phouanavong, S., Wan, K., Yu, C., Lewis, S.E., Rubin, G.M.
 and Celinker, S.

TITLE
JOURNAL

COMMENT

Direct Submission
 Submitted (18-DEC-2001) Berkeley Drosophila Genome Project,
 Lawrence Berkeley National Laboratory, One Cyclotron Road,
 Berkeley, CA 94720, USA
 Sequence submitted by:
 Berkeley Drosophila Genome Project
 Lawrence Berkeley National Laboratory
 Berkeley, CA 94720
 This clone was sequenced as part of a high-throughput process to
 sequence clones from Drosophila Gene Collection 1 (Rubin et al.,
 Science 2000). The sequence has been subjected to integrity checks
 for sequence accuracy, presence of a polyA tail and contiguity
 within 100 kb in the genome. Thus we believe the sequence to
 reflect accurately this particular cDNA clone. However, there are
 artifacts associated with the generation of cDNA clones that may
 have not been detected in our initial analyses such as internal
 priming, priming from contaminating genomic DNA, retained introns
 due to reverse transcription of unspliced precursor RNAs, and
 reverse transcriptase errors that result in single base changes.
 For further information about this sequence, including its location
 and relationship to other sequences, please visit our web site
 (<http://fruitfly.berkeley.edu>) or send email to
cdna@fruitfly.berkeley.edu.

FEATURES

source

Location/Qualifiers
 1..1981

gene

CDS

/organism="Drosophila melanogaster"
 /strain="y; cn bw sp"
 /db_xref="taxon:7227"
 /map="67E5-67E5"
 1..1981
 /gene="CG11811"
 /note="alignment with genomic scaffold AE003547"
 /db_xref="FLYBASE:FBgn0036099"
 506..1207
 /gene="CG11811"
 /note="Longest ORF"
 /codon_start=1
 /product="GH06691p"
 /protein_id="AAL8457.1"
 /db_xref="GI:17944781"
 /db_xref="FLYBASE:FBgn0036099"
 /translation="MISPLFVNALSSSSSSAASLTSKMTAPGRPLVLCGPS
 GSGCKTLKRFAPFSPGFSISHTKREBEQGVHYVEREMAAIAGGEFT
 EFAETGVLVGTGSKAAVREIQAGRCVITIDIEKGVQIKRPDLPVILFNPSIKK
 LERLRKSGSTESLSKRLNAQVEIDVLTGNGHKLINNDVIDVAEERFNVVO
 ELKEQKQGVSVNLN"

BASE COUNT
ORIGIN

Query Match 4.9%; Score 44; DB 3; Length 1981;
 Best Local Similarity 100.0%; Pred. No. 7.1e-11;
 Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 855 CCGGGTAAAAA
 Db 1909 CCGGGTAAAAA

RESULT 3
 LOCUS AX187087 293 bp DNA linear PAT 06-AUG-2001
 DEFINITION Sequence 2782 from Patent WO0142467.
 ACCESSION AX187087
 VERSION AX187087.1 GI:15138532
 KEYWORDS human.
 SOURCE Homo sapiens
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE

1 (bases 1 to 293)
 Schleigel, R., Deeds, D., Berger, A. and Zhao, X.
 Genes, compositions, kits, and methods for identification,
 assessment, prevention, and therapy of cervical cancer

```

JOURNAL Patent: WO 0142467-A 2782 14-JUN-2001;
          Millennium Predictive Medicine, Inc. (US)
FEATURES Location/Qualifiers
          source
            1..293
              /organism="Homo sapiens"
              /db_xref="taxon:9606"
BASE COUNT 54 a 80 c 11 g 148 t
ORIGIN
Query Match 4.8%; Score 43; DB 6; Length 293;
Best Local Similarity 100.0%; Pred. No. 2.3e-10;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 856 GGGTAAAAA... 898
Db 96 GGGTAAAAA... 54

RESULT 4
LOCUS AF043538 1032 bp mRNA linear PLN 18-AUG-1998
DEFINITION Arabidopsis thaliana 20S proteasome beta subunit PBG1 (PBG1) mRNA,
ACCESSION AF043538
VERSION AF043538.1 GI:3421122
KEYWORDS Arabidopsis thaliana.
SOURCE Arabidopsis thaliana.
ORGANISM Arabidopsis thaliana.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1 (bases 1 to 1032)
AUTHORS Fu, H., Doelling, J.H., Arendt, C.S., Hochstrasser, M. and
Vierstra, R.D.
Molecular organization of the 20S proteasome gene family from
Arabidopsis thaliana
Genetics 149 (2), 677-692 (1998)
JOURNAL MEDLINE 98278790
PUBMED 9611183
REFERENCE 2 (bases 1 to 1032)
AUTHORS Fu, H.
TITLE Direct Submission
JOURNAL Submitted (20-JAN-1998) Horticulture, U. of Wisconsin, 1575 Linden
Dr., Madison, WI 53706, USA
FEATURES Location/Qualifiers
          source
            1..1032
              /organism="Arabidopsis thaliana"
              /strain="Columbia"
              /db_xref="taxon:3702"
              /clone="147M2117"
            1..1032
              /gene="PBG1"
            43..783
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              /gene="PBG1"
              /BC_number="3.4.99.46"
              /codon_start=1
              /product="20S proteasome beta subunit PBG1"
              /protein_id="AAC32074.1"
              /db_xref="GI:3421123"
              /transcript="MTTFSVPIDNDGSMKLAEEBSORTIYPYTGTSVAIKKXGVL
              MASDMSGSGSTIRKNTKRYKAKGKSLGASGEISDPEILRYADELTLNMDD
              GNSLGPKEHNHTLVRYNRRKRPPLNNTLYVGGVANKGSIQAMSMIGVSEDDHY
              ATGFNHNLRPLTRDEWHADLSFEDGKLEKCKRVLLYRDRSAINKLQIAKITEBSV
              TVSQPSIKTYEFSFNPPTAGAGSW"
BASE COUNT 343 a 178 c 227 g 284 t
ORIGIN
Query Match 4.8%; Score 43; DB 8; Length 1032;
Best Local Similarity 100.0%; Pred. No. 2.3e-10;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 856 GGGTAAAAA... 898
Db 96 GGGTAAAAA... 54

JOURNAL Patent: WO 0142467-A 2782 14-JUN-2001;
          Millennium Predictive Medicine, Inc. (US)
FEATURES Location/Qualifiers
          source
            1..293
              /organism="Homo sapiens"
              /db_xref="taxon:9606"
BASE COUNT 54 a 80 c 11 g 148 t
ORIGIN
Query Match 4.8%; Score 43; DB 6; Length 293;
Best Local Similarity 100.0%; Pred. No. 2.3e-10;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 856 GGGTAAAAA... 898
Db 96 GGGTAAAAA... 54

RESULT 5
LOCUS AX053122 1091 bp DNA linear PAT 13-JAN-2001
DEFINITION Sequence 1 from Patent WO0073470.
ACCESSION AX053122
VERSION AX053122.1 GI:12227487
KEYWORDS Zea mays.
SOURCE Zea mays.
ORGANISM Zea mays.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
Clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 1091)
AUTHORS Simmons, C.R.
TITLE Endo- and exo-glucanase polynucleotides and methods of use
JOURNAL PIONEER HI-BRED INTERNATIONAL, INC. (US)
LOCATION/Qualifiers
          source
            1..1091
              /organism="Zea mays"
              /db_xref="taxon:4577"
              /note="unnamed protein product"
              /codon_start=1
              /protein_id="CAC21954.1"
              /db_xref="GI:12227488"
              /translation="MPSSACVLCIAAVIAAAATTAHSCGLDNPDRSIGRQLA
              EAGRVHDLPGGIRAAVSGAASSRAVNIASDFVEAPLKLQIVDKAKAGRYVVP
              DFLKGDYLDLDRKNFTMLEAHSSRAVEDAKDPLFAALKKESVAVGGVCGKLSYE
              VGKSDVKAACLSHPYSVTADMRKYEKMTIELIGANDITTEPKREYFEVYLERHE
              VPFRRQDRDGPRLHGLVQAOALNEACFARTRLNSINHSVAIVCFEDSWLPRLIFM
              ATTSITVILIFVSMYFSEFLFAVL"
BASE COUNT 299 a 297 c 276 g 219 t
ORIGIN
Query Match 4.8%; Score 43; DB 6; Length 1091;
Best Local Similarity 100.0%; Pred. No. 2.3e-10;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 856 GGGTAAAAA... 898
Db 999 GGGTAAAAA... 1041

RESULT 6
LOCUS BC004060 1303 bp mRNA linear ROD 07-AUG-2002
DEFINITION Mus musculus, clone MGC:6174 IMAGE:3590170, mRNA, complete cds.
ACCESSION BC004060
VERSION BC004060.1 GI:13278527
KEYWORDS MGC.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 1303)
AUTHORS Strausberg, R.
TITLE Direct Submission
JOURNAL Submitted (28-FEB-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomes Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT Contact: MGC help desk
Email: gcrp@nci.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305

```

Web site: <http://www.sngc.stanford.edu>
Contact: (Dickson, Mark) md@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAC Plate: 11 Row: c Column: 5.

FEATURES
source

Source

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source
1. .1303
/organism="Mus musculus"
/db_xref="taxon:10090"
/map="CZECH lit"
/clone="MGC:8174 IMAGE:3590170"
/tissue_type="Mammary tumor metastatized to lung. Tumor
arose spontaneously from a senescent normal mammary
(clonal) outgrowth infected with the virus MMV."
/clone_lib="NCI CGAP_Lu29"
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6"
162. .839
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BASE COUNT
ORIGIN

280 a 365 c 324 g 334 t

Query Match	4.8%	Score 43;	DB 10;	Length 1303;
Best Local Similarity	100.0%;	Pred. No. 2.3e-10;		
Matches 43;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	856	GGGTAAAAAAAAAAAAAAAAAAAAAAAAA	898
Db	1248	GGGTAAAAAAAAAAAAAAAAAAAAAAAAA	1290

RESULT	7	
LOCUS	HSMB02527	
DEFINITION	HSMB02527	1445 bp linear
ACCESSION	AL162008	PRI 23-MAR-2000
VERSION	AL162008.1	DKFZ586C2017 (from DKFZ586C2017).
KEYWORDS		
SOURCE	Homo sapiens.	

FEATURES
SOURCE

Source

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location/Qualifiers
1. 1445
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="DKFZp586C2017"
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/tissue_type="uterus"
/clone_id="586 (synonym: hut1)". Vector pSport1; host
DH10B; sites NotI + SalI/MluI
/dev_stage="adult"
/dev_age="1"

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polyA_signal	1342.	1347	
polyA_site	1361		
BASE COUNT	523 a	206 c	232 g 484 t
ORIGIN			

Query Match 4.8%; Score 43; DB 9; Length 1445;
Best Local Similarity 100.0%; Pred. No. 2.3e-10;
Matches 43; Conservative 0; Mismatches 0; Indels 0;
Gaps 0.

QY	856 GCGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	898
Db	1358 GCGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	1400

RESULT 8	BC005424	1463 bp	mRNA	linear	ROD 07-AUG-2005
LOCUS	BC005424				
DEFINITION	Mus musculus, tumor susceptibility gene 101, clone MGC:5785				
ACCESSION	BC005424				
VERSION	BC005424.1				
KEYWORDS	MGC.				
SOURCE	house mouse.				
ORGANISM	Mus musculus.				

JOURNAL
Submitted (27-MAR-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-7590,
USA
REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
COMMENT Contact: MGC help desk

FEATURES

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/BLINL at: <http://image.llnl.gov>

Series: IRK Plate: 7 Row: 5 Column: 24

This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 11230779.

Location/Qualifiers

FEATURES

SOURCE

Source


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NDGSSRELVNLTGCTIPVRSGNIVNIPICMLDTPYNPICFVKPTSSMTIKTKH
VDANKTILPYLHDMKPRSELLEIOMIYFGEPPVSRPTVSAVSPYATGPP
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DGTISEDTJASLISVSKLWKNRKEEDGQAOALNLTAKTEEDLKGOKLEEWY
RLOEVAEVDKRNLELKKDELSALKRMEQSNNDIDVILLPTAPLKKQILNLTA
EENAIEDTIFYLEALRNGVIDLVFLKRVHLSRKKOFLRMAIMOKARKTAGSLDY"

BASE COUNT      451 a      342 c      313 g      357 t
ORIGIN

Query Match      4.8%; Score 43; DB 10; Length 1463;
Best Local Similarity 100.0%; Pred. No. 2.3e-10;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      856 GGGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 898
Db      1407 GGGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1449

RESULT 9
LOCUS      AR202048      1835 bp      DNA      linear      PAT 20-APR-2002
DEFINITION Sequence 1 from patent US 6361948.
ACCESSION  AR202048
VERSION     AR202048.1 GI:20256587
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 1835)
AUTHORS    Triccoli, V. and Roudine, R.
TITLE      Prognostic compositions for prostate cancer and methods of use
           thereof
JOURNAL     Patent: US 6361948-A 1 26-MAR-2002;
FEATURES
source      1. 1835
           Location/Qualifiers
BASE COUNT      384 a      607 c      514 g      330 t
ORIGIN

Query Match      4.8%; Score 43; DB 6; Length 1835;
Best Local Similarity 100.0%; Pred. No. 2.2e-10;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      856 GGGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 898
Db      1749 GGGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1791

RESULT 10
LOCUS      HSU58996      1853 bp      mRNA      linear      PRI 10-OCT-2001
DEFINITION Homo sapiens testis calpastatin mRNA, complete cds.
ACCESSION  U58996
VERSION     U58996.2 GI:5042381
KEYWORDS
SOURCE      Homo sapiens.
ORGANISM    Homo sapiens.
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE   1 (bases 1 to 1853)
AUTHORS    Li, S., Liang, Z. G., Wang, G. Y., Yavetz, B., Kim, E. D. and Goldberg, E.
TITLE      Molecular cloning and characterization of functional domains of a
           human testis-specific isoform of calpastatin
JOURNAL     Biol. Reprod. 63 (1), 172-178 (2000)
MEDLINE     20318416
PUBMED      10859257
REFERENCE   2 (bases 1 to 1853)
AUTHORS    O'Hern, P. A., Liang, Z. G., Wang, G. Y., Yavetz, B., Kim, E. and
           Goldberg, E.
TITLE      A Novel Testis-specific Isoform of Calpastatin Detected with Serum
           from an Infertile Patient
JOURNAL     Unpublished
REFERENCE   3 (bases 1 to 1853)

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AUTHORS      O'Hern, P. A., Liang, Z. G., Wang, G. Y., Yavetz, B., Kim, E. and
           Goldberg, E.
TITLE      Direct Submission
JOURNAL     Submitted (22-MAY-1996) Department of Biochemistry, Molecular
           Biology and Cell Biology, Northwestern University, 2153 Sheridan
           Road, Evanston, IL 60208, USA
REFERENCE   4 (bases 1 to 1853)
AUTHORS      Goldberg, E.
TITLE      Direct Submission
JOURNAL     Submitted (15-APR-1998) Department of Biochemistry, Molecular
           Biology and Cell Biology, Northwestern University, 2153 Sheridan
           Road, Evanston, IL 60208, USA
REMARK      5 (bases 1 to 1853)
AUTHORS      Goldberg, E.
TITLE      Direct Submission
JOURNAL     Submitted (21-APR-1998) Department of Biochemistry, Molecular
           Biology and Cell Biology, Northwestern University, 2153 Sheridan
           Road, Evanston, IL 60208, USA
REMARK      6 (bases 1 to 1853)
AUTHORS      Goldberg, E.
TITLE      Direct Submission
JOURNAL     Submitted (11-JUN-1999) Department of Biochemistry, Molecular
           Biology and Cell Biology, Northwestern University, 2153 Sheridan
           Road, Evanston, IL 60208, USA
REMARK      Sequence update by submitter
           On Jun 11, 1999 this sequence version replaced gi:3068549.
FEATURES
source      1. 1853
           Location/Qualifiers
CDS
note="t:CAST; testis specific isoform of calpastatin"
/protein_id="A014353.1"
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/translation="MGQFLSTFLEGGSPATVWHDKLCGERGAREAVRIPOQAKK
EERLEKGGEDETIPSEYRLKPAIDDKGKPLPEPEEKPRRSSELIDLSDFDS
ECKEKPEPEKEEESKAAAPAVSAVSKTSCIGNAPPEPTLIGTYPDNAVEL
ADSLGKREADPEGKPYMDKRVKAKAEDEKREKERTIPDTRLEVKONDKPUL
PKESKEQLPMSDDYTLDAISDFSGPQNASLTKEDAKLAALISEVSSQTPASTQA
GAPPRDTSQDLDLDAIDKLSDSLQRODPDENKPMEDKVKERAKAHRHDKGERD
TIPPEYRHLLDDNGQDKPVKPKKSEDSKPADQDDIDALSGDLDCSPSTYETSON
TAKDKCKKAASSSKAPKNGKANDSAKTETSKPKD"
misc_feature 67..190
note="encodes amino acids unique to testis isoform"
BASE COUNT      674 a      370 c      412 g      397 t
ORIGIN

Query Match      4.8%; Score 43; DB 9; Length 1853;
Best Local Similarity 100.0%; Pred. No. 2.2e-10;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      856 GGGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 898
Db      1771 GGGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1813

RESULT 11
LOCUS      BC003999      1913 bp      mRNA      linear      ROD 07-AUG-2002
DEFINITION Mus musculus, clone MGC:7540 IMAGE:3492402, mRNA, complete cds.
ACCESSION  BC003999
VERSION     BC003999.2 GI:16306793
KEYWORDS
SOURCE      house mouse.
ORGANISM    Mus musculus
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

REFERENCE 1 (bases 1 to 1913)
 AUTHORS Strausberg, R.
 TITLE Direct Submission
 JOURNAL Submitted (28-FEB-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
 REMARK NIH-MGC Project URL: <http://imgc.nci.nih.gov>
 On Oct 22, 2001 this sequence version replaced gi:13278363.
 CONTACT: MGC help desk
 E-mail: cgaps-tr@mail.nih.gov
 Tissue Procurement: Gilbert Smith, Ph.D.
 DNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: The I.M.A.G.E. Consortium (ILLUM)
 Center, Stanford University School of Medicine, Stanford, CA 94305
 Web site: <http://www.shgc.stanford.edu>
 CONTACT: (Dickson, Mark) mdickpaxil.stanford.edu
 Dickson, M., Schmitz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILLUM at: <http://image.llnl.gov>
 Series: IRAC Plate: 8 Row: h Column: 7.
 Location/Qualifiers
 1. 1913
 /organism="Mus musculus"
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 /map="C2BCH II"
 /clone="MGC:7540 IMAGE:3492402"
 /tissue_type="Mammary tumor metastasized to lung. Tumor arose spontaneously from a senescent normal mammary (clonal) outgrowth infected with the virus MMTV."
 /clone_lib="MCL CGAP_Lu29"
 /lab_host="DH10B"
 /note="Vector: PCMV-SPORT6"
 129. 1205
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 CDS
 BASE COUNT 576 a 401 c 508 g 428 t
 ORIGIN

Query Match 4.88; Score 43; DB 10; Length 1913;
 Best Local Similarity 100.0%; Pred. No. 2.2e-10;
 Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 856 GGGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 898
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 Db 1834 GGGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1876

RESULT 12
 SSA293335 2668 bp mRNA linear VRT 15-JUL-2002
 LOCUS Salmo salar mRNA for putative Interleukin-1 receptor type I (11-1a1 gene)
 ACCESSION AJ293335
 VERSION AJ293335.1 GI:19912978
 KEYWORDS IL-1RL gene; Interleukin-1 receptor-like protein.
 SOURCE Atlantic salmon.
 ORGANISM Salmo salar
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei;

REFERENCE 1
 AUTHORS Cunnigham, C., Stansberg, C., Olsen, L., Zou, J., Secombes, C. J. and Dev. Comp. Immunol. 26 (5), 415-431 (2002)
 JOURNAL 21904083
 TITLE Cloning of a Salmo salar interleukin-1 receptor-like cDNA
 MEDLINE 21904083
 REFERENCE 2 (bases 1 to 2668)
 AUTHORS Subramaniam, S.
 TITLE Direct Submission
 JOURNAL Submitted (13-SEP-2000) Subramaniam S., Molecular Immunology, Sars International Centre for Marine Molecular Biology, Bergen High Technology Centre, Thormohlenstgt. 55, Bergen, N-5008, NORWAY

FEATURES
 source
 1. 2668
 /organism="Salmo salar"
 /db_xref="taxon:8030"
 /clone="pSS211"
 /tissue_type="head kidney"
 /dev_stage="young adult"
 /lab_host="E. coli"
 /country="Norway:Bergen"
 1. 2668
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 1. .92
 /gene="IL-1RL"
 93. 1808
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 /function="Immune response"
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 /db_xref="GI:19912979"
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 156. 1805
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 polyA_signal 2594. 2600
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 BASE COUNT 734 a 577 c 645 g 712 t
 ORIGIN

Query Match 4.88; Score 43; DB 5; Length 2668;
 Best Local Similarity 100.0%; Pred. No. 2.2e-10;
 Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 856 GGGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 898
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 Db 2615 GGGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2657

RESULT 13
 AF069757 3280 bp DNA linear INV 28-MAY-1999
 LOCUS Dictyostellium discoideum spermidine synthase gene, complete cds.
 ACCESSION AF069757
 VERSION AF069757.1 GI:4903272

reverse transcriptase errors that result in single base changes.
For further information about this sequence, including its location
and relationship to other sequences, please visit our Web site
(<http://fruitfly.berkeley.edu>) or send email to
cdna@fruitfly.berkeley.edu.

FEATURES

source

gene

CDS

1. 5012
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/map="100D2-100D2"
1. 5012
/gene="CG1815"
/note="alignment with genomic scaffold AE003779"
/db_xref="FLYBASE:FBgn0039863"
160. 2883
/gene="CG1815"
/note="longest ORF"
/codon_start=1
/product="SD07276p"
/protein_id="AAL3986.1"
/db_xref="GI:17862984"
/db_xref="FLYBASE:FBgn0039863"
/translation="MAFEDGERLANLNAEDRNIVPAYSMATRCRSRKTLSNSMGN
DDGPRRSNLRSENEEFKHNAPLDRIIHDDRESELALNTSGESSLFSADDTKT
TTAKTPEEEAERIALIVEEPTPGMDPPCKCGCKLMPGSKLRSPHSCYRPAAT
TKEDSSMKGCECVTAAPKRLRNGVSDLLSOLLSPALDPMKHVGAHRLSPLEV
FPIYTKKFTPNVYFESLACITRNAGYSTDEFLSEVKIIOHNLIIIDAGDAKYEAS
KAVKVCROFANEIDTCPECYLNANSSDWEVVCGRPHLLMLAKLGFPYPAKAMG
SSNSTLVNAFEGKHDAFVPAKDFLYSAQPNPTQTSRSARDLAECIREVELIHD
IKRKIGAFNAPRYRTPDLEQOOLEQMPGVAIDRELEPANKTPIQLIRKTD
DKLSIVKTKATSCNEDSPSPKTLSEVNVSVTGSGCSDHSNVKSNVYEYSRS
GESLTSRCVGLKRSKLAKIYASVETSEAVAPRKHSLSDSFTSESEHRRKSK
HARKHONDNOIEEAETKGOEPPSPITSKONEMLRDEENVITENANDTSASPVSA
SVYSVIEVPRRGVYITKIPREOCQTAEDTAAPRIPIPTAPPRKNIPIKGNPAAPK
QSDVERQOELIKKVIPIETIKTEVASEPDDEGIEASPAHQPTDQVYQOETITQ
PESOMPAAPAPQPKPVNDAPVEEVRIKEELISEDEMETESIVSRKLSVPPPLPM
PPPPPLPRESPATADSVRFVGDYTIQVYHRHPLQTRPFCOPHLRLRHOSQLAR
ILLASHRLRHRPRESLRHTNFEEKTIVSOPPHRRLHQPTRLCSDPTW"

BASE COUNT 1485 a 1346 c 1135 g 1046 t
ORIGIN

Query Match 4.8%; Score 43; DB 3; length 5012;
Best Local Similarity 100.0%; Pred. No. 2.1e-10;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 856 GGGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 898
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DB 4961 GGGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 5003

Search completed: February 22, 2003, 05:26:00
Job time : 2547.4 secs

GenCore version 5.1.4.P5_4578
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OM nucleic - nucleic search, using sw model

Run on: February 22, 2003, 04:08:26 ; Search time 88.6106 Seconds
(Without alignments) 5691.782 Million cell updates/sec

Title: US-09-832-320-1

Perfect score: 898
Sequence: 1 ctgcgacgactctgcgacgctc.....aaaaaaaaaaaaaaaaaaaaa 898

Scoring table: OLIGO_MNC
Gapop 60.0 , Gapext 60.0

Searched: 442118 seqs, 280819700 residues

Word size : 25

Total number of hits satisfying chosen parameters: 12207

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : Published Applications_NA:*

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5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
10: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	898	100.0	898	10	US-09-832-320-1
2	612	68.2	612	10	US-09-832-320-3
3	43	4.8	447	10	US-09-770-444-759
4	43	4.8	1077	9	US-09-764-868-497
5	42	4.7	111	10	US-09-925-299-635
6	42	4.7	365	10	US-09-960-352-5456
7	42	4.7	495	10	US-09-864-761-1723
8	42	4.7	595	10	US-09-867-552A-31
9	42	4.7	707	10	US-09-764-864-19
10	42	4.7	938	10	US-09-037-657-16
11	42	4.7	1041	10	US-09-925-300-440
12	42	4.7	1119	9	US-09-796-753-133
13	42	4.7	1267	10	US-09-925-301-188
14	42	4.7	1300	10	US-09-822-849A-3
15	42	4.7	1431	10	US-09-764-864-695
16	42	4.7	1436	9	US-09-764-864-272
17	42	4.7	1659	10	US-09-796-692-667
18	42	4.7	1686	10	US-09-925-301-157
19	42	4.7	1711	10	US-09-935-390A-17

20	42	4.7	1824	10	US-09-814-786-1	Sequence 1, Appl1
21	42	4.7	1877	12	US-10-007-399-2	Sequence 2, Appl1
22	42	4.7	2104	10	US-09-925-300-288	Sequence 288, App
23	42	4.7	2519	12	US-10-139-262-9	Sequence 9, Appl1
24	42	4.7	3084	10	US-09-764-864-89	Sequence 89, Appl1
25	42	4.7	3397	10	US-09-925-301-414	Sequence 414, App
26	42	4.7	5354	9	US-09-815-923-1	Sequence 1, Appl1
27	41	4.6	112	9	US-09-768-827-51	Sequence 51, Appl1
28	41	4.6	185	9	US-10-046-935-1615	Sequence 1615, Ap
29	41	4.6	185	9	US-09-878-178-1615	Sequence 1615, Ap
30	41	4.6	202	10	US-09-925-299-573	Sequence 573, App
31	41	4.6	211	10	US-09-867-701-2599	Sequence 2599, Ap
32	41	4.6	217	10	US-09-867-574-13266	Sequence 12266, Ap
33	41	4.6	255	10	US-09-878-574-13064	Sequence 13064, A
34	41	4.6	276	10	US-09-878-574-14211	Sequence 14211, A
35	41	4.6	292	10	US-09-960-352-12176	Sequence 12176, A
36	41	4.6	302	10	US-09-925-299-710	Sequence 710, App
37	41	4.6	308	9	US-09-954-531-79	Sequence 79, Appl1
38	41	4.6	317	10	US-09-954-531-263	Sequence 263, App
39	41	4.6	317	10	US-09-960-352-3366	Sequence 3366, Ap
40	41	4.6	376	9	US-09-933-797-343	Sequence 343, App
41	41	4.6	383	10	US-09-960-352-5366	Sequence 5366, Ap
42	41	4.6	418	10	US-09-960-352-10650	Sequence 10650, A
43	41	4.6	444	10	US-09-960-352-1281	Sequence 1281, Ap
44	41	4.6	456	10	US-09-960-352-9659	Sequence 9659, Ap
45	41	4.6	523	10	US-09-962-436-68	Sequence 68, Appl1

ALIGNMENTS

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RESULT 1
US-09-832-320-1
; Sequence 1, Application US/09832320
; Patent No. US20010049834A1
; GENERAL INFORMATION:
; APPLICANT: Crane, Edmund H.
; APPLICANT: Crane, Virginia C.
; TITLE OF INVENTION: Polynucleotide and Methods of Use
; FILE REFERENCE: 35718/214291
; CURRENT APPLICATION NUMBER: US/09/832,320
; CURRENT FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: US 60/195,801
; PRIOR FILING DATE: 2000-04-10
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 898
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (63)...(674)
US-09-832-320-1

Query Match      100.0%  Score 898:  DB 10:  Length 898:
Best Local Similarity 100.0%  Pred. No. 8.1e-299:
Matches 898:  Conservative 0:  Mismatches 0:  Indels 0:  Gaps 0;
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OY 1 CTGCAGCGACTCTGCAGCGCTCATCTGAGCCATTTAGTCAGATCAACCACTCCAGATCT 60
DB 1 CTGCAGCGACTCTGCAGCGCTCATCTGAGCCATTTAGTCAGATCAACCACTCCAGATCT 60
OY 61 CATGCGGACGCTCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 120
DB 61 CATGCGGACGCTCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 120
OY 121 CGTGTCTTCTCTCTGCGACCCCTCTCTGCGCTCTGCGCGCGCGCGCGCGCGCGCGG 180
DB 121 CGTGTCTTCTCTCTGCGACCCCTCTCTGCGCTCTGCGCGCGCGCGCGCGCGCGCGG 180
OY 181 CCGGCGTCTCTATGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 240
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Db 181 CCGGGTCTATGCGGGGCGGGGGGGGAGCCACAGGCGGAGCGC 240
Oy 241 GCAGGAGGAGCAAGCGAGCGGAGAGTACTGCGCGCCAGACAGGCGCGG 300
Db 241 GCAGGAGGAGCAAGCGAGCGGAGAGTACTGCGCGCCAGACAGGCGCGG 300
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Oy 421 GCGGCAACCAAGGGGTGGGCGAGTACGCGCGCGCCCGCGAGTGGCGCTG 480
Db 421 GCGGCAACCAAGGGGTGGGCGAGTACGCGCGCGCCCGCGAGTGGCGCTG 480
Oy 481 TGGCGGAGGCGGCTACTACACCCAGCCAGACAGTGGCGCGCGGGGCGAGT 540
Db 481 TGGCGGAGGCGGCTACTACACCCAGCCAGACAGTGGCGCGCGGGGCGAGT 540
Oy 541 GCAGCTACACGAGGTGGTGGCGCAACACCGCGAGTGGCGCGCGAGCGCT 600
Db 541 GCAGCTACACGAGGTGGTGGCGCAACACCGCGAGTGGCGCGCGAGCGCT 600
Oy 601 GCGGCAAGGGGCGCGAGTGGTGGCGCAACACCGCGAGTGGCGCGAGCG 660
Db 601 GCGGCAAGGGGCGCGAGTGGTGGCGCAACACCGCGAGTGGCGCGAGCG 660
Oy 661 AGAGCCCTACTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAG 720
Db 661 AGAGCCCTACTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAG 720
Oy 721 CCGGGGAGGAGGAGTACTAGTGGTTCATAGTCTTCTAGTGGCGAGGAG 780
Db 721 CCGGGGAGGAGGAGTACTAGTGGTTCATAGTCTTCTAGTGGCGAGGAG 780
Oy 781 TTTTGTGTGATCGGCTGGTCTTCTTGTGTGGACAACTGTTGTTGTGTA 840
Db 781 TTTTGTGTGATCGGCTGGTCTTCTTGTGTGGACAACTGTTGTTGTGTA 840
Oy 841 TCAGCTTTTGTGGCGGGTAAAAA 898
Db 841 TCAGCTTTTGTGGCGGGTAAAAA 898
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RESULT 2
US-09-832-320-3
; Sequence 3, Application US/09832320
; Patent No. US20010049834A1

GENERAL INFORMATION:

APPLICANT: Crane, Edmund H.
APPLICANT: Crane, Virginia C.
TITLE OF INVENTION: Mice Pathogenesis-Related
FILE REFERENCE: 35718/214291
CURRENT APPLICATION NUMBER: US/09/832,320
PRIOR FILING DATE: 2001-04-10
PRIOR APPLICATION NUMBER: US 60/195,801
NUMBER OF SEQ ID NOS: 3
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 612
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(612)
US-09-832-320-3

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Query Match 68.2%; Score 612; DB 10; Length 612;  
Best Local Similarity 100.0%; Pred. No. 5,1e-201;  
Matches 612; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 63 ATGGGCGATCGGCGAGCGACACACACCTCTCTGCTGCGCGCGGCGCAATGGGCGAGG 122  
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Oy 123 TGTCTGTCTGTGCGACCTCTGCGCTGTGCGCGCGCGGCGCGACCGAGCGCG 182  
Db 61 TGTCTGTCTGTGCGACCTCTGCGCTGTGCGCGCGCGGCGCGACCGAGCGCG 120  
Oy 183 GCGGCTCATGCGGGGCGGCGGGGTGACCAAGCGGAGCGAGTGGCGACCGGCG 242  
Db 121 GCGGCTCATGCGGGGCGGCGGGGTGACCAAGCGGAGCGAGTGGCGACCGGCG 180  
Oy 243 AGCGGCAACAGCGGAGCGGCGAGTACTGCGCGCGCGCAACAGGAGCGCGCGG 302  
Db 181 AGCGGCAACAGCGGAGCGGCGAGTACTGCGCGCGCGCAACAGGAGCGCGGCG 240  
Oy 303 GTGGGCGTGGCGCGCGCTGCGGTGGAACGCGGCGCTGCGCGCGCGCGGAGAGT 362  
Db 241 GTGGGCGTGGCGCGCGCTGCGGTGGAACGCGGCGCTGCGCGCGCGCGGAGAGT 300  
Oy 363 GCGGAGCGCGCGGCGAGGCGGCGTGGCGGTGCGCGAGCTGGGCGGCGACCCCTACG 422  
Db 301 GCGGAGCGCGCGGCGAGGCGGCGTGGCGGTGCGCGAGCTGGGCGGCGACCCCTACG 360  
Oy 423 GCGAACCAGGGGCGGCGAGTACCGCGCGCGCGCGCGAGTGGTGGCGCTGGTGG 482  
Db 361 GCGAACCAGGGGCGGCGAGTACCGCGCGCGCGCGCGAGTGGTGGCGCTGGTGG 420  
Oy 483 GCGGAGGGGCGTACTACACCGCAACACAGTGGCGCGCGCGGCGGCGAGTGGCG 542  
Db 421 GCGGAGGGGCGTACTACACCGCAACACAGTGGCGCGCGCGGCGGCGAGTGGCG 480  
Oy 543 AGCTACACGCGAGTGGTGGCGCAACAGCGCGAGTGGCGCGCGAGCGACACTG 602  
Db 481 AGCTACACGCGAGTGGTGGCGCAACAGCGCGAGTGGCGCGCGAGCGACACTG 540  
Oy 603 GCGAGGCGGCGCGAGCTACGCTGTGCTGTACAAACCGCGAGGCAACGTGCGAGG 662  
Db 541 GCGAGGCGGCGCGAGCTACGCTGTGCTGTACAAACCGCGAGGCAACGTGCGAGG 600  
Oy 663 AGCCCTACTAG 674  
Db 601 AGCCCTACTAG 612
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RESULT 3
US-09-770-444-759/C
; Sequence 759, Application US/09770444
; Patent No. US20020023280A1

GENERAL INFORMATION:

APPLICANT: Goriach, Jörn
APPLICANT: An, Yong-Qiang
APPLICANT: Hamilton, Carol M.
APPLICANT: Price, Jennifer L.
APPLICANT: Raines, Tracy M.
APPLICANT: Yu, Yang
APPLICANT: Rameaka, Joshua G.
APPLICANT: Page, Amy
APPLICANT: Matthew, Abraham V.
APPLICANT: Ledford, Brooke L.
APPLICANT: Moessner, Jeffrey P.
APPLICANT: Haas, William David
APPLICANT: Garcia, Carlos A.
APPLICANT: Krieker, Maya
APPLICANT: Slader, Ted
APPLICANT: Davis, Keith R.
APPLICANT: Allen, Keith
APPLICANT: Hoffman, Neil
APPLICANT: Hurban, Patrick

```

; TITLE OF INVENTION: Expressed Sequences of Arabidopsis
; FILE REFERENCE: Chailana
; CURRENT APPLICATION NUMBER: US/09/770,444
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/178,502
; PRIOR FILING DATE: 2000-01-27
; NUMBER OF SEQ ID NOS: 999
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 759
; LENGTH: 447
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-770-444-759

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Query Match
Best Local Similarity 100.0%; Score 43; DB 10; Length 447;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 856 GCGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 898
Db 74 GCGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 32

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RESULT 4
US-09-764-868-497
; Sequence 497, Application US/09764868
; Patent No. US2002016871A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT32
; CURRENT APPLICATION NUMBER: US/09/764,868
; PRIOR FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1510
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 497
; LENGTH: 1077
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-868-497

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Query Match
Best Local Similarity 100.0%; Score 43; DB 9; Length 1077;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 856 GCGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 898
Db 1026 GCGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1068

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RESULT 5
US-09-925-299-635
; Sequence 635, Application US/09925299
; Patent No. US20020055627A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA102
; CURRENT APPLICATION NUMBER: US/09/925,299
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05883
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1556
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 635
; LENGTH: 111
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:

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; NAME/KEY: misc_feature
; LOCATION: (11)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (19)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (24)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (35)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (38)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (109)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-925-299-635

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Query Match
Best Local Similarity 100.0%; Score 42; DB 10; Length 111;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 856 GCGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 897
Db 58 GCGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 99

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RESULT 6
US-09-960-352-5456
; Sequence 5456, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Mengping
; APPLICANT: Byatt, John C.
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; PRIOR FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 5456
; LENGTH: 365
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 24-BOWMS1-009-Q1-E1-F7
US-09-960-352-5456

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Query Match
Best Local Similarity 100.0%; Score 42; DB 10; Length 365;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 857 GGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 898
Db 18 GGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 59

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RESULT 7
US-09-864-761-1723
; Sequence 1723, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
; FILE REFERENCE: Acomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761

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CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
SEQ ID NO 1723
LENGTH: 495
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC011347.1
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.9
OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 4
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.2
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.6
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 4.3
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 3.8
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.7
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.7
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 2.1
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2
US-09-864-761-1723

Query Match 4.7%; Score 42; DB 10; Length 495;
Best Local Similarity 100.0%; Pred. No. 3.6e-06;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 857 GGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 898
Db 234 GGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 275
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RESULT 8
US-09-967-552A-31
Sequence 31, Application US/09967552A
Patent No. US20020124282A1
GENERAL INFORMATION:
APPLICANT: Danilevskaya, Olga
APPLICANT: Butler, Karlene H.
```

```

APPLICANT: Miao, Guo-Hua
APPLICANT: Morgante, Michele
APPLICANT: Sakai, Hajime
APPLICANT: Simmons, Carl R.
APPLICANT: Wang, Zude
APPLICANT: Famodu, Omolayo
APPLICANT: Hantke, Sabine
TITLE OF INVENTION: Plant Reproduction Polynucleotides and Methods of Use
FILE REFERENCE: DD0010R
CURRENT APPLICATION NUMBER: US/09/967,552A
CURRENT FILING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: PCT/US00/23735
PRIOR FILING DATE: 2000-08-30
PRIOR APPLICATION NUMBER: US 60/151,575
PRIOR FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 82
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 31
LENGTH: 595
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(360)
US-09-967-552A-31
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Query Match 4.7%; Score 42; DB 10; Length 595;
Best Local Similarity 100.0%; Pred. No. 3.4e-06;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 857 GGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 898
Db 525 GGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 566
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```

RESULT 9
US-09-764-864-19
Sequence 19, Application US/09764864
Patent No. US20020132753A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PT23
CURRENT APPLICATION NUMBER: US/09/764,864
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 1792
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 19
LENGTH: 707
TYPE: DNA
ORGANISM: Homo sapiens
US-09-764-864-19
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Query Match 4.7%; Score 42; DB 10; Length 707;
Best Local Similarity 100.0%; Pred. No. 3.3e-06;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 857 GGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 898
Db 634 GGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 675
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RESULT 10
US-09-037-657-16
Sequence 16, Application US/09037657A
Patent No. US20020045741A1
GENERAL INFORMATION:
APPLICANT: Hilton, Douglas J.
APPLICANT: Nicola, Nicos A.
APPLICANT: Farley, Allison
APPLICANT: Wilson, Tracy
APPLICANT: Zhang, Jian-Guo
```



```

; APPLICANT: Alexander, Warren
; APPLICANT: Rakar, Steven
; APPLICANT: Fabri, Louis
; APPLICANT: Kojima, Tetsuo
; APPLICANT: Maeda, Masatsugu
; APPLICANT: Kikuchi, Yasufumi
; APPLICANT: Nash, Andrew
; TITLE OF INVENTION: A NOVEL HAEMPOIETIN RECEPTOR AND GENETIC SEQUENCES
; FILE REFERENCE: DAVIES COLLISON CAVE (CIP)
; CURRENT APPLICATION NUMBER: US/09/037,657A
; CURRENT FILING DATE: 1998-03-10
; EARLIER APPLICATION NUMBER: 08/928,720
; EARLIER FILING DATE: 1997-09-11
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 938
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(465)
; OTHER INFORMATION: Description of Unknown Organism: Murine NR6.3
US-09-037-657-16
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Query Match          4.7%; Score 42; DB 10; Length 938;
Best Local Similarity 100.0%; Pred. No. 3e-06;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY 857 GGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 898
Db 884 GGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 925
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RESULT 11
US-09-925-300-440
; Sequence 440, Application US/09925300
; Patent No. US20020151681A1
; GENERAL INFORMATION:
; APPLICANT: Craig Rosen,
; APPLICANT: Steve Ruben
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA101
; CURRENT APPLICATION NUMBER: US/09/925,300
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCI/US00/05988
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1890
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 440
; LENGTH: 1041
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1025)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (1030)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (1039)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-925-300-440
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Query Match          4.7%; Score 42; DB 10; Length 1041;
Best Local Similarity 100.0%; Pred. No. 3e-06;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY 857 GGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 898
Db 979 GGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1020
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RESULT 12
US-09-796-753-133
; Sequence 133, Application US/09796753
; Publication No. US20030027998A1
; GENERAL INFORMATION:
; APPLICANT: McCarthy, Sean A.
; TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
; FILE REFERENCE: 7853-227-999
; CURRENT APPLICATION NUMBER: US/09/796,753
; CURRENT FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 09/183,175
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: 09/223,094
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 09/223,546
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 09/224,246
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 09/259,388
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/122,458
; PRIOR FILING DATE: 1999-03-01
; PRIOR APPLICATION NUMBER: 09/312,359
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 09/336,536
; PRIOR FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: 09/342,687
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: 09/345,464
; PRIOR FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: 09/365,164
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: 09/399,723
; PRIOR FILING DATE: 1999-09-20
; PRIOR APPLICATION NUMBER: 09/409,634
; PRIOR FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: 09/471,179
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 09/474,071
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: 09/474,072
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: 09/514,010
; PRIOR FILING DATE: 2000-02-25
; PRIOR APPLICATION NUMBER: 09/516,745
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 09/572,002
; PRIOR FILING DATE: 2000-05-14
; PRIOR APPLICATION NUMBER: 09/597,993
; PRIOR FILING DATE: 2000-06-19
; PRIOR APPLICATION NUMBER: 09/599,596
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 09/630,334
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: 09/606,565
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: 09/606,317
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: 09/665,666
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: 09/677,751
; PRIOR FILING DATE: 2000-09-30
; NUMBER OF SEQ ID NOS: 162
; SEQ ID NO 133
; LENGTH: 1119
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-796-753-133
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Query Match
Best Local Similarity 100.0%; Score 42; DB 9; Length 1119;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 857 GGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 898
DB 1040 GGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1081

RESULT 13
US-09-925-301-188
; Sequence 188, Application US/09925301
; Patent No. US20020052308A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA106
; CURRENT APPLICATION NUMBER: US/09/925,301
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05862
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1694
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 188
; LENGTH: 1267
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (12)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (25)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-925-301-188

Query Match
Best Local Similarity 100.0%; Score 42; DB 10; Length 1267;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 857 GGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 898
DB 1195 GGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1236

RESULT 14
US-09-822-849A-3
; Sequence 3, Application US/09822849A
; Patent No. US20020045170A1
; GENERAL INFORMATION:
; APPLICANT: Wong, Gordon G.
; APPLICANT: Clark, Hilary
; APPLICANT: Fechtel, Kim
; APPLICANT: Agostino, Michael J.
; APPLICANT: Howes, Steven H.
; APPLICANT: Resnick, Richard J.
; APPLICANT: Gulukota, Kamalakari
; APPLICANT: Graham, James R.
; APPLICANT: Genetics Institute, Inc.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS
; FILE REFERENCE: GIN 6403
; CURRENT APPLICATION NUMBER: US/09/822,849A
; CURRENT FILING DATE: 2001-09-04
; PRIOR APPLICATION NUMBER: 60/195,582
; PRIOR FILING DATE: 2000-04-06
; NUMBER OF SEQ ID NOS: 598
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1300
; TYPE: DNA
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; ORGANISM: Homo sapiens
US-09-822-849A-3

Query Match
Best Local Similarity 100.0%; Score 42; DB 10; Length 1300;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 857 GGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 898
DB 1232 GGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1273

RESULT 15
US-09-764-864-695
; Sequence 695, Application US/09764864
; Patent No. US20020132753A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT223
; CURRENT APPLICATION NUMBER: US/09/764,864
; CURRENT FILING DATE: 2001-01-17
; PRIOR APPLICATION data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1792
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 695
; LENGTH: 1431
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-864-695

Query Match
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Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 857 GGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 898
DB 1390 GGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1431

Search completed: February 22, 2003, 06:10:54
Job time : 100.611 secs
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2	75	12.3	286	10	BE512404	BE512404 946070F0
3	50	8.2	352	13	BM101325	BM101325 EBP101_SC
4	50	8.2	996	12	BG343259	BG343259 HVSME9000
5	40	6.5	681	9	AU082529	AU082529 AU082529
6	35	5.7	253	9	AU029886	AU029886 AU029886

SOURCE Zea mays

/note="Vector: lambdaZAP; Site_1: EcoRI; Site_2: XhoI; Plants were grown in the greenhouse at the University of California, Riverside (Fenton, su close, ty close). Whole spike with awns trimmed were collected at white, green and yellow anther stages (Fenton). Total RNA was prepared from each pool, equal quantities of all three RNA pools were combined, poly(A) RNA was purified from the mixture, one primary unamplified cDNA library was made, and 1 million pfu were in vivo excised to give pluscript SK(-) cDNA phagemids. These steps were performed in the ty close lab (choi) at the University of California, Riverside. Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Frisch, Atkins and Wing) Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or above. For more details on library preparation and sequence analysis see <http://www.genome.clemson.edu/projects/barley>. To order this clone see <http://www.genome.clemson.edu/orders> Also see Close ty, Wing R, Kleinhofs A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (<http://wheat.pw.usda.gov/g9pages/bgn/31/cover.html>)"

BASE COUNT 183 a 310 c 377 g 123 t 3 others

ORIGIN

Query Match 8.2%; Score 50; DB 12; Length 996;
Best Local Similarity 100.0%; Pred. No. 2.7e-11;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 346 GCCAGCCCTACGCGGCGAGCGGCTACCGCGCGCC 395
|||||
DB 399 GCCAGCCCTACGCGGCGAGCGGCTACCGCGCGCC 448

RESULT 5
A0082529 681 bp mRNA linear EST 02-APR-2002
LOCUS A0082529 Rice panicle shorter than 3cm Oryza sativa (japonica
DEFINITION cultivar-group) cDNA clone E30820, mRNA sequence.

ACCESSION A0082529
VERSION A0082529.1 GI:6984553
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group).
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 681)
AUTHORS Sasaki,T. and Yamamoto, K.
TITLE Rice cDNA from panicle (2000)
JOURNAL Unpublished (2000)
COMMENT Contact: Takuji Sasaki
National Institute of Agrobiological Resources
Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki
305-8602, Japan
Tel: 81-298-38-7441
Fax: 81-298-38-7468
Email: tsasaki@r.affrc.go.jp, URL:<http://rpg.dna.affrc.go.jp/>
PROJECT "RGP"

FEATURES
source location/Qualifiers
1..681
/organism="Oryza sativa (japonica cultivar-group)"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone="E30820"
/clone_1lb="Rice panicle shorter than 3cm"
/dev_stage="shorter than 3cm"
/note="Organ: panicle"
BASE COUNT 136 a 187 c 214 g 141 t 3 others
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 5.4e-07;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 571 TACAACCCGACGCGACGTCAGGCGGAGCCCTACT 610
|||||
DB 287 TACAACCCGACGCGACGTCAGGCGGAGCCCTACT 326

RESULT 6
A0029886 293 bp mRNA linear EST 01-APR-2002
LOCUS A0029886 Rice cDNA from immature leaf including apical meristem
DEFINITION Oryza sativa (japonica cultivar-group) cDNA clone E50124_1A, mRNA
sequence.

ACCESSION A0029886
VERSION A0029886
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group).
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 293)
AUTHORS Sasaki,T. and Yamamoto, K.
TITLE Rice cDNA from immature leaf including apical meristem
JOURNAL Unpublished (1997)
COMMENT Contact: Takuji Sasaki
National Institute of Agrobiological Resources
Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki
305-8602, Japan
Tel: 81-298-38-7441
Fax: 81-298-38-7468
Email: tsasaki@r.affrc.go.jp, URL:<http://rpg.dna.affrc.go.jp/>
PROJECT "RGP"

FEATURES
source location/Qualifiers
1..293
/organism="Oryza sativa (japonica cultivar-group)"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone="E50124_1A"
/clone_1lb="Rice cDNA from immature leaf including apical
meristem"
/dev_stage="immature"
/note="Organ: leaf; immature leaf including apical
meristem (under long day condition)"
BASE COUNT 49 a 102 c 107 g 33 t 2 others
ORIGIN

Query Match 5.7%; Score 35; DB 9; Length 293;
Best Local Similarity 100.0%; Pred. No. 7.4e-05;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 351 CCCCTACGCGCGAAGCGGCTGCGAGCTACC 385
|||||
DB 33 CCCCTACGCGCGAAGCGGCTGCGAGCTACC 67

RESULT 7
BE125871 288 bp mRNA linear EST 19-JUL-2000
LOCUS BE125871 Sorghum bicolor cDNA, mRNA
DEFINITION BE1_59_A04.D1_A002 Dark Grown 1 (DGL) Sorghum bicolor cDNA, mRNA
sequence.

ACCESSION BE125871
VERSION BE125871.1 GI:8548461
KEYWORDS EST.
SOURCE Sorghum.
ORGANISM Sorghum bicolor
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Sorghum.

REFERENCE 1 (bases 1 to 288)
 AUTHORS Cordonnier-Pratt,M.-M., Gingle,A., Marsala,C., Sudman,M. and Pratt
 ,L.H.
 TITLE An EST database from Sorghum: dark-grown seedlings
 JOURNAL Unpublished (2000)
 COMMENT Contact: Cordonnier-Pratt MM
 Laboratory for Genomics and Bioinformatics
 The University of Georgia, Department of Plant Biology
 Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
 Tel: 706 542 1860
 Fax: 706 583 0210
 Email: mmpratt@uga.edu

Sequences have been trimmed to exclude PolyA, vector and regions
 below Phred quality 16. The threshold for highest quality sequence
 is 20.

Seq primer: JEN REV
 High quality sequence stop: 285
 POLYA-No.

FEATURES
 SOURCE Location/Qualifiers
 1..288
 /organism="Sorghum bicolor"
 /db_xref="taxon:4558"
 /clone_lib="Dark Grown 1 (DG1)"
 /note="Organ: 5-day-old dark-grown seedlings; Vector:
 lambda zap; Site_1: XhoI; Site_2: EcoRI; The library was
 made from poly-A RNA in the cloning vector lambda Zap II.
 Clones to be sequenced were prepared by mass excision."

BASE COUNT 46 a 123 c 76 g 42 t
 ORIGIN 1 others

Query Match 5.1%; Score 31; DB 10; Length 288;
 Best Local Similarity 100.0%; Pred. No. 0.0039;

Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 78 CCTCTCGCGCTCGCGCGCGCGCGCGCG 108
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 Db 193 CCTCTCGCGCTCGCGCGCGCGCGCGCG 223

Search completed: February 22, 2003, 06:06:24
 Job time : 988.279 secs

[illegible]

RESULT 2

ID ABA96417 standard; cDNA; 898 BP.

AC ABA96417;

DT 02-APR-2002 (first entry)

DE Maize PR1-C10 encoding CDNA SEQ ID NO 1.

KW malze; pathogen-related; PR1-C10; plant; transgenic; gene; ss.

Zea mays.

FH	Key	Location/Qualifiers
EE	and	53 574

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ET      /*tag= a
ET      /tag= a

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XX
PN
TTS3001049834-A1

XX
PD
06-DEC-2001

XX
XX
10-APR-2001: 2001TTS-0832320

10-APR-2000: 2000US-195801P.

AA
PA
(CRAN/) CRANE E H.

(CHAIN) CHAINS A C

XX

XX : 07-08-2019

DR P-PSDB; AAM48742.

PT New nucleic acid encoding a pathogen-related protein isolated from

PT enhanced disease resistance

PS Claim 1; Page 30-31; 34pp; English.

CC The invention relates to an isolated nucleic acid encoding a

cc plants for enhanced disease resistance

Sequence 898 BP; 161 A; 295 C; 309 G; 133 T; 0 other;

Query Match	100.0%;	Score 612;	DB 24;	Length 898;
Best Local Similarity	100.0%;	Pred NO	2	1e-250.

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Matches 612; conservative 0; mismatches 0; indels 0; gaps 0;
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Db	63	ATTGGCGACTCGCGGACGACACACACACTCTCTCTCTCCCGCGCCATGGCCACGGCG	122
QY	61	TGCTTGCTCTCTGCCACACCTCTCTGGCCTTGGCGCGCGCGCGCCGACCCACGCGCG	120
Db	123	TGCTTGCTCTCTCGCCACACCTCTCTCGCCTCTGGCGCGCGCGCCGACCCACGCGCGCG	182
QY	121	CGGCTCTCATGCGCGGCGCGGCGCGGCGCGGTACCAAGCGCACGAGGTTGGACCGGCG	180
Db	183	CGGCTCTCATGCGCGGCGCGGCGCGGCGCGGTACCAAGCGCACGAGGTTGGACCGGCG	242
QY	181	AGCGGACGACACGCGACGCGCGGAGTACTGTGCGCGCACAAACGAGCGCGCGCGCG	240
Db	243	AGCGGACGACACGCGACGCGCGGAGTACTGTGCGCGCACAAACGAGCGCGCGCGCG	302
QY	241	GTTGGGCGTGGCCCGCTCGGTGGAGACGCGGCGCTTGCGCGCGCGCGCGGAGACGTTG	300
Db	303	GTTGGGCGTGGCCCGCTCGGTGGAGACGCGGCGCTTGCGCGCGCGCGCGGAGACGTTG	362
QY	301	GCGCAGCAGCGCGCGACGAGGCGGCGTGCCTGTCGCGGACGTGGCGGCGCCAGCCCTACGGC	360
Db	363	GCGCAGCAGCGCGCGACGAGGCGGCGTGCCTGTCGCGGACGTGGCGGCGCCAGCCCTACGGC	422
QY	361	GCGAACCGAGGCGTGGGCGCACTACCGCGCGCGCCCGCCGAGGTGTGGCGCTGTGGGTG	420
Db	423	GCGAACCGAGGCGTGGGCGCACTACCGCGCGCGCCCGCCGAGGTGTGGCGCTGTGGGTG	482
QY	421	GCGAGAGGCGGTACTTACACCCAGCGCCAAACAGACGTGGCGCGCGGCGGCGAGTGGCGC	480
Db	483	GCGAGAGGCGGTACTTACACCCAGCGCCAAACAGACGTGGCGCGCGGCGGCGAGTGGCGC	542
QY	481	ACGTACACCGAGGTGTGTGGCGCAACCGCGGAGGTGCGGGTGGCGCGACGCTGC	540
Db	543	ACGTACACCGAGGTGTGTGGCGCAACCGCGGAGGTGCGGGTGGCGCGACGCTGC	602
QY	541	GCGACGCGCGCACGCTACGCTTGCTGTACAAACCGACAGGACAGTGCAGGCGCAG	600
Db	603	GCGACGCGCGCACGCTACGCTTGCTGTACAAACCGACAGGACAGTGCAGGCGCAG	662
QY	601	AGCCCTCTAG 612	
Db	663	AGCCCTCTAG 674	

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Job time : 158.877 secs

Job time : 158.877 secs

GenCore version 5.1.4.p5 4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 22, 2003, 04:08:26 ; Search time 60.3894 Seconds

(without alignments)
5691.782 Million cell updates/sec

Title: US-09-832-320-3

Perfect score: 612
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Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 44218 seqs, 280819700 residues

Word size : 25

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: listing first 45 summaries

Database : Published_Applications_NA:*

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Prod. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
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2	612	100.0	898	10	US-09-832-320-1

ALIGNMENTS

RESULT 1
US-09-832-320-3
; Sequence 3, Application US/09832320
; Patent No. US20010049834A1
; GENERAL INFORMATION:
; APPLICANT: Crane, Edmund H.
; APPLICANT: Crane, Virginia C.
; TITLE OF INVENTION: Maize Pathogenesis-Related
; FILE REFERENCE: 35718/214291
; CURRENT APPLICATION NUMBER: US/09/832,320
; CURRENT FILING DATE: 2001-04-10

PRIOR APPLICATION NUMBER: US 60/195,801
; PRIOR FILING DATE: 2000-04-10
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 612
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(612)
US-09-832-320-3

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Best Local Similarity 100.0%; Prod. No. 2.9e-266;
Matches 612; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	ATGGGCGACATCGCGAGCGACACACACCTCTGCTCCCGCGCCATGAGCGAGCG	60
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QY	61	TGCTTGTCTTCTTCTGCGACCTCTGCTGCGCGCGCGCGCGCGCGCGCGCGCG	120
DB	61	TGCTTGTCTTCTGCGACCTCTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	120
QY	121	CGCTCTCTATGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	180
DB	121	CGCTCTCTATGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	180
QY	181	AGCGGCGACGACGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	240
DB	181	AGCGGCGACGACGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	240
QY	241	GTGGGCGTGGCG	300
DB	241	GTGGGCGTGGCG	300
QY	301	GGCGGCGAGCG	360
DB	301	GGCGGCGAGCG	360
QY	361	GGGACGAGGCGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	420
DB	361	GGGACGAGGCGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	420
QY	421	GGGAGGCGGCGTATACACCGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	480
DB	421	GGGAGGCGGCGTATACACCGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	480
QY	481	ACGTACGCGCAGTGTGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	540
DB	481	ACGTACGCGCAGTGTGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	540
QY	541	GGCAGGCGGCG	600
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US-09-832-320-1
; Sequence 1, Application US/09832320
; Patent No. US20010049834A1
; GENERAL INFORMATION:
; APPLICANT: Crane, Edmund H.
; APPLICANT: Crane, Virginia C.
; TITLE OF INVENTION: Maize Pathogenesis-Related
; FILE REFERENCE: 35718/214291
; CURRENT APPLICATION NUMBER: US/09/832,320

GenCore version 5.1.4.p5.4578
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Run on: February 22, 2003, 03:01:40 ; Search time 77 seconds
(without alignments)
808.511 Million cell updates/sec

Title: US-09-832-320-2

Sequence: 1 MAHRSHHHLLLPAPMATA.....ATLTCLYPNHGNOGOSPY 203

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Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-LOOPTXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blomsun62 -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR.SCORE=pct -THR.MAX=100 -THR.MIN=0 -ALIGN=15
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-WARN.TIMEDOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database:

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3: /cgn2_6/ptodata/1/ina/6A.COMB.seq:*
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5: /cgn2_6/ptodata/1/ina/PTDS.COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	304	28.0	771	1	US-08-181-271A-10
3	304	28.0	771	1	US-08-449-315-10
4	304	28.0	771	1	US-08-444-803-10
5	304	28.0	771	1	US-08-449-043-10
6	304	28.0	771	1	US-08-456-265A-10
7	304	28.0	771	1	US-08-455-416-10
8	304	28.0	771	1	US-08-455-244-10
9	304	28.0	771	1	US-08-454-876-10
10	304	28.0	771	2	US-08-457-364-10
11	304	28.0	771	2	US-08-456-262-10
12	304	28.0	771	2	US-08-456-240-10

13	304	28.0	771	2	US-08-455-736-10	Sequence 10, Appl
14	304	28.0	771	4	US-09-350-600-10	Sequence 10, Appl
15	304	28.0	771	4	US-08-181-271A-10	Sequence 10, Appl
16	286	27.3	696	1	US-08-449-315-11	Sequence 11, Appl
17	286	27.3	696	1	US-08-449-043-11	Sequence 11, Appl
18	286	27.3	696	1	US-08-449-043-11	Sequence 11, Appl
19	286	27.3	696	1	US-08-456-265A-11	Sequence 11, Appl
20	286	27.3	696	1	US-08-455-416-11	Sequence 11, Appl
21	286	27.3	696	1	US-08-455-244-11	Sequence 11, Appl
22	286	27.3	696	1	US-08-454-876-11	Sequence 11, Appl
23	286	27.3	696	2	US-08-457-364-11	Sequence 11, Appl
24	286	27.3	696	2	US-08-456-262-11	Sequence 11, Appl
25	286	27.3	696	2	US-08-456-240-11	Sequence 11, Appl
26	286	27.3	696	2	US-08-455-736-11	Sequence 11, Appl
27	286	27.3	696	2	US-08-457-364-11	Sequence 11, Appl
28	286	27.3	696	2	US-08-455-244-11	Sequence 11, Appl
29	286	27.3	696	4	US-09-350-600-11	Sequence 11, Appl
30	286	27.3	696	4	US-09-257-583-6	Sequence 6, Appl
31	286	26.5	860	1	US-08-181-271A-33	Sequence 33, Appl
32	286	26.5	860	1	US-08-449-315-33	Sequence 33, Appl
33	286	26.5	860	1	US-08-444-803-33	Sequence 33, Appl
34	286	26.5	860	1	US-08-449-043-33	Sequence 33, Appl
35	286	26.5	860	1	US-08-456-265A-33	Sequence 33, Appl
36	286	26.5	860	1	US-08-455-416-33	Sequence 33, Appl
37	286	26.5	860	1	US-08-455-244-33	Sequence 33, Appl
38	286	26.5	860	1	US-08-454-876-33	Sequence 33, Appl
39	286	26.5	860	2	US-08-457-364-33	Sequence 33, Appl
40	286	26.5	860	2	US-08-456-262-33	Sequence 33, Appl
41	286	26.5	860	2	US-08-456-240-33	Sequence 33, Appl
42	286	26.5	860	2	US-08-455-736-33	Sequence 33, Appl
43	286	26.5	860	2	US-08-457-364-33	Sequence 33, Appl
44	286	26.5	860	4	US-09-350-600-33	Sequence 9, Appl
45	286	26.4	809	1	US-08-181-271A-9	Sequence 9, Appl

ALIGNMENTS

RESULT 1
US-09-257-583-12
; Sequence 12, Application US/09257583A
; Patent No. 6429362
; GENERAL INFORMATION:
; APPLICANT: Crane, Virginia
; TITLE OF INVENTION: Family of Maize PR-1 Genes And Promoters
; FILE REFERENCE: 5718-32, 035718/175219
; CURRENT APPLICATION NUMBER: US/09/257,583A
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 749
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (92)..(583)
US-09-257-583-12

Alignment Scores:

Pred. No.: 1,14e-19
Score: 333.00
Percent Similarity: 48.13%
Best Local Similarity: 37.65%
Query Match: 30.69%
DB: 4
Gaps: 8
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QY 16 ---Prometala-----ThralAcysleuLeuLeuAlaThrlleuLeuAlaLeuCysAla 32

DB 86 CAACAAATGACGACGAGGTGCTCCCTAGCTGCTGCGCATGCGCATGCTGCTG 145
OY 33 AAlaProAlaProThrHisGlyAlaArgValLeuMetProGlyGlyAlaValAlaThr 52
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OY 53 LysAlaGlnGlnGlyThrGlySerGlySerAsnAlaThrAlaAspGluTyrLeuAla 72
DB 155 -----ACGCCCGCAACCTGCGCGCAGAC---TAGGTGAC 167
OY 73 ProHisGlnAlaAlaArgAlaAlaValGlyValAlaProLeuAlaGTPAsnAlaGlyLeu 92
DB 188 CCGCACACACCG 247
OY 93 AlaserAlaAlaAlaGlyThrValAlaGlnGlnAlaArgArgGlnGlyGlyCysAlaPheAla 112
DB 248 GCGCGCGTACCGCGACGACGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 301
OY 113 AspValGlyAlaSerProTyrGlyAlaAsnGlnGlyTyrPalAsnTyrArgAla----- 130
DB 302 CACTCCCGC---GGCCCTACCGCGCGACCTTCTGCGCGCGCGCGCGCGCGCGCGCG 358
OY 131 ArgProAlaGluValAlaAlaLeuTyrValAlaGlnGlyArgTyrTyrThrHisAlaAsn 150
DB 359 TCGGCGTCCGACG 418
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OY 171 AlaGluValGlyCysAlaGlnAlaSerCysAlaThrGlyAla---ThLeuThrLeuGly 189
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DB 539 AGCTACACCG 580

RESULT 2
US-08-181-271A-10
Sequence 10. Application US/08181271A
Patent No. 5614395

GENERAL INFORMATION:
APPLICANT: Ryals, John A.
APPLICANT: Alexander, Danny C.
APPLICANT: Beck, James J.
APPLICANT: Duesing, John H.
APPLICANT: Friedlich, Leslie B.
APPLICANT: Goodman, Robert M.
APPLICANT: Harms, Christian
APPLICANT: Meins, Jr., Frederick
APPLICANT: Montoya, Alice
APPLICANT: Moyer, Mary B.
APPLICANT: Neuhaus, Jean-Marc
APPLICANT: Payne, George B.
APPLICANT: Sperison, Christoph
APPLICANT: Stinson, Jeffrey R.
APPLICANT: Umes, Scott J.
APPLICANT: Ward, Eric R.
APPLICANT: Williams, Shericea C.
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: CIBA-GEIGY Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: New York
COUNTRY: USA
ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/181,271A
FILING DATE: 13-JAN-94
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/093,301
FILING DATE: 16-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/937,197
FILING DATE: 6-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/678,378
FILING DATE: 1-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/305,566
FILING DATE: 6-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/165,667
FILING DATE: 8-MAR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/042,847
FILING DATE: 6-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/632,441
FILING DATE: 21-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/425,504
FILING DATE: 20-OCT-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/848,506
FILING DATE: 6-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/768,122
FILING DATE: 27-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/580,431
FILING DATE: 7-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/368,672
FILING DATE: 20-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/329,018
FILING DATE: 24-MAR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/045,957
FILING DATE: 12-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8614
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 771 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-181-271A-10

Alignment Scores:
Pred. No.: 3 12e-17 Length: 771
Score: 304.00 Matches: 64
Percent Similarity: 56.55% Conservative: 18
Best Local Similarity: 44.14% Mismatches: 57
Query Match: 28.02% Indels: 6
DB: 1 Gaps: 3

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Db 171 GTAGGGGTGGAAACCATTAATCTTGGGACACAGGGGTGACAGCCCTATGACAAATTAATGTT 230
QY 101 AlaGlnGlnAlaArgGlnGlnGlyGlyCysAlaAlaProAlaAspValGlyAlaSerProTyrGly 120
Db 231 TGTCAATTTGGCTGCGAGACTGCAACCTGTGCATTTGCAT---GGCCAAATACGGC 261
QY 121 AlaAsn-----GlnGlyTyrAlaSerTyrAlaArgProAlaGluValValAlaLeu 138
Db 282 GAAAAACCTGACCTCAGAGAAAGTGGCGATTATTATGACG---GCTGCTAAGGCGCTGCAGATG 338
QY 139 TyrValAlaGlnGlyAlaArgTyrTyrThrHISAlaAsnAspThrCysAlaAlaGlyValGln 158
Db 339 TGGGTGCATGAAACCATTAATCTTGGGACACAGGGGTGACAGCCCTATGACAAATTAATGTT 398
QY 159 CysGlyThrTyrThrGlnValValTyrArgAsnThrAlaGlyValGlyCysAlaGlnAla 178
Db 399 TGTGACACATTAATCTCAGAGTGGTGTGGCGTAACTGCTGTGGATGTGCTAAGGTT 458
QY 179 SerCysAlaThrGlyAlaThrLeuThrCysLeuTyrAsnProHISGlyAsnValGln 198
Db 459 AAGTGCACAAATGGAGCAATATGTTGCTCTTGCACAACTATGATCTCCAGATTAATGTCATA 518
QY 199 GlyGlnSerProTyr 203
Db 519 GGCCAAAGTCCATAC 533

RESULT 3
US-08-449-315-10
US-08-449-315-10
Sequence 10. Application US/08449315
Patent No. 5650505
GENERAL INFORMATION:
APPLICANT: Ryals, John A.
APPLICANT: Alexander, Danny C.
APPLICANT: Beck, James J.
APPLICANT: Duesing, John H.
APPLICANT: Friedrich, Leslie B.
APPLICANT: Goodman, Robert M.
APPLICANT: Harms, Christian
APPLICANT: Weins, Jr., Frederick
APPLICANT: Montoya, Alice
APPLICANT: Moyer, Mary B.
APPLICANT: Neuhaus, Jean-Marc
APPLICANT: Payne, George B.
APPLICANT: Sperison, Christoph
APPLICANT: Stinson, Jeffrey R.
APPLICANT: Dknes, Scott J.
APPLICANT: Ward, Eric R.
APPLICANT: Williams, Shericea C.
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
NUMBER OF INVENTION: DNA SEQUENCES AND USES THEREOF
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: CIBA-GEIGY Corporation
STREET: 7 skyline Drive
CITY: Hawthorne
STATE: New York
COUNTRY: USA
ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOOS
SOFTWARE: Patentin release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/449, 315

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      1  FILING DATE: 24-MAY-1995
      2  CLASSIFICATION: 800
      3  PRIOR APPLICATION DATA:
      4  APPLICATION NUMBER: 08/181,271
      5  FILING DATE: 13-JAN-94
      6  APPLICATION NUMBER: US 08/093,301
      7  FILING DATE: 16-JUL-1993
      8  PRIOR APPLICATION DATA:
      9  APPLICATION NUMBER: US 07/937,197
     10  FILING DATE: 6-NOV-1992
     11  PRIOR APPLICATION DATA:
     12  APPLICATION NUMBER: US 07/678,378
     13  FILING DATE: 1-APR-1991
     14  PRIOR APPLICATION DATA:
     15  APPLICATION NUMBER: US 07/305,566
     16  FILING DATE: 6-FEB-1989
     17  PRIOR APPLICATION DATA:
     18  APPLICATION NUMBER: US 07/165,667
     19  FILING DATE: 8-MAR-1988
     20  PRIOR APPLICATION DATA:
     21  APPLICATION NUMBER: US 08/042,847
     22  FILING DATE: 6-APR-1993
     23  PRIOR APPLICATION DATA:
     24  APPLICATION NUMBER: US 07/632,441
     25  FILING DATE: 21-DEC-1990
     26  PRIOR APPLICATION DATA:
     27  APPLICATION NUMBER: US 07/425,504
     28  FILING DATE: 20-OCT-1989
     29  PRIOR APPLICATION DATA:
     30  APPLICATION NUMBER: US 07/848,506
     31  FILING DATE: 6-MAR-1992
     32  PRIOR APPLICATION DATA:
     33  APPLICATION NUMBER: US 07/768,122
     34  FILING DATE: 27-SEP-1991
     35  PRIOR APPLICATION DATA:
     36  APPLICATION NUMBER: US 07/580,431
     37  FILING DATE: 7-SEP-1990
     38  PRIOR APPLICATION DATA:
     39  APPLICATION NUMBER: US 07/368,672
     40  FILING DATE: 20-JUN-1989
     41  PRIOR APPLICATION DATA:
     42  APPLICATION NUMBER: US 07/329,018
     43  FILING DATE: 24-MAR-1989
     44  PRIOR APPLICATION DATA:
     45  APPLICATION NUMBER: US 08/045,957
     46  FILING DATE: 12-APR-1993
     47  ATTORNEY/AGENT INFORMATION:
     48  NAME: Elmer, James Scott
     49  REGISTRATION NUMBER: 36,129
     50  REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727
     51  TELECOMMUNICATION INFORMATION:
     52  TELEPHONE: (919)541-8614
     53  TELEFAX: (919)541-8689
     54  INFORMATION FOR SEQ ID NO: 10:
     55  SEQUENCE CHARACTERISTICS:
     56  LENGTH: 771 base pairs
     57  TYPE: nucleic acid
     58  STRANDEDNESS: single
     59  TOPOLOGY: linear
     60  MOLECULE TYPE: cDNA
     61  US-08-449-315-10
  
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QY 81 ValGlyValAlaProLeuArgTrpAsnAlaGlyLeuAlaSerAlaAlaGlyThrVal 100
DB 171 GTAGCGGTGGAACCTTACTTGGACACAGGGGTAGACGCTTGCACAAATATGCTT 230
QY 101 AlagIngluArgAlaGlyGlyCysAlaPheAlaAspValGlyAlaSerProTyrGly 120
DB 231 TCTCAATGGCTGCAGACTGCACAACTCTGACATCTCAT-----GGCCAAATACGCC 281
QY 121 AlaAsp-----GlnGlyTrpAlaSerTyrArgAlaArgProAlaGlyValValAlaLeu 138
DB 282 GAAACCTAGCTAGGAGAGAGTGGCATTTTATGAGC---GCTGCTAAGCGCGTGCAGATG 338
QY 139 TrpValAlaGluGlyArgTyrTrpHisAlaAsnThrCysAlaAlaGlyArgGln 158
DB 339 TGGGTGCTGATGAGAAAGTATGATGACCTCAATCTTGTGCACACAGGACAGGTG 398
QY 159 CysGlyThrTyrThrGlnValAlaTrpArgAsnThrAlaGluValGlyCysAlaGln 178
DB 399 TGTGGACACTATACCTGAGTGGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 458
QY 179 SerCysAlaThrGlyAlaThrLeuThrLeuCysLeuTyrAsnProHisGlyAsnValGln 198
DB 459 AAGTGCACAAATGGAGGATATGTGTCTGCTGCACTATGATCTCTCAGATGATGATA 518
QY 199 GlyGlnSerProTyr 203
DB 519 GGCCAAAGTCCATAC 533

RESULT 4
US-08-444-803-10
Sequence 10, Application US/08444803
Patent No. 5654414

GENERAL INFORMATION:

APPLICANT: Ryals, John A.
APPLICANT: Alexander, Danny C.
APPLICANT: Beck, James J.
APPLICANT: Duesing, John H.
APPLICANT: Friedrich, Leslie B.
APPLICANT: Goodman, Robert M.
APPLICANT: Harms, Christian
APPLICANT: Hains, Jr., Frederick
APPLICANT: Montoya, Alice
APPLICANT: Moyer, Mary B.
APPLICANT: Neuhaus, Jean-Marc
APPLICANT: Payne, George B.
APPLICANT: Sperison, Christoph
APPLICANT: Stinson, Jeffrey R.
APPLICANT: Ukes, Scott J.
APPLICANT: Ward, Eric R.
APPLICANT: Williams, Shericoa C.
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: CIBA-GEIGY Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: New York
COUNTRY: USA
ZIP: 10532

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/444,803
FILING DATE: 19-MAY-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/181,271
FILING DATE: 13-JAN-94
APPLICATION NUMBER: US 08/093,301
FILING DATE: 16-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/937,197
FILING DATE: 6-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/678,378
FILING DATE: 1-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/305,566
FILING DATE: 6-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/165,667
FILING DATE: 8-MAR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/042,847
FILING DATE: 6-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/632,441
FILING DATE: 21-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/425,504
FILING DATE: 20-OCT-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/848,506
FILING DATE: 6-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/368,672
FILING DATE: 20-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/329,018
FILING DATE: 24-MAR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/045,957
FILING DATE: 12-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8614
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 771 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-444-803-10

Alignment Scores:

Pred. No.: 3.12e-17 Length: 771
Score: 304.00 Matches: 64
Percent Similarity: 56.55% Conservative: 18
Best Local Similarity: 44.14% Mismatches: 57
Query Match: 28.02% Indels: 6
DB: 1 Gaps: 3

US-09-832-320-2 (1-203) x US-08-444-803-10 (1-771)

QY 61 SerGlySerAsnAlaThrAlaAspGlyTyrLeuAlaProHisAsnGlnAlaArgAla 80
DB 111 TCTCATGCCCAAACTCTCAACAAAGCTATTGTGATGCCCATTAACACAGCTGTGCAGAT 170

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QY 81 ValGlyValAlaProLeuArgTrpAsnAlaGlyLeuAlaSerAlaAlaGlyThrVal 100
Db 171 GTAGGGCTGGACCATTAACCTGGACAAAGGGGTAGACCTATGACAAATAATGTT 230
QY 101 AlAGlnGlnArgTrpGlnGlyGlyCysAlaPheAlaAspValGlyLaserProTyrGly 120
Db 231 TCTCAATTGGCTGACAGCTGCAACCTGTCATCTCAT-----GGCAATACGGC 281
QY 121 AlaAsn-----GlnGlyTrpAlaSerTyrArgAlaArgProAlaGlyValAlaAla 138
Db 282 GAAACCTTACCTCAGGGAAGTGGCGAATTTATACG---CCTCTTAAGCCCGTCGAGATG 338
QY 139 TrpValAlaGlnGlyArgTyrTyrThrHisAlaAsnThrCysAlaAlaGlyArgGln 158
Db 339 TGGGTGATGACAAAGCTACTATGACCAACTCAATAATCTGTGCACAGACAGCGTG 398
QY 159 CysGlyThrTyrThrGlnValValTrpArgAsnThrAlaGlnValGlyCysAlaGlnAla 178
Db 399 TGTGGACACTATCTACGAGGTGGTTGGCGTACTGCGTTCGTGTGATGCTAGGGAT 458
QY 179 SerCysAlaThrGlyAlaThrLeuThrLeuCysLeuTyrAsnProHisGlyAsnValGln 198
Db 459 AAGTGCACAACTGAGAGATATGTGTCTTGTGCACTATGATGCTCCAGTATATGCATA 518
QY 199 GlyLaserProTyr 203
Db 519 GGCCAAAGTCCATAC 533

RESULT 5
US-08-449-043-10
; Sequence 10, Application US/08449043
; Patent No. 5689044
GENERAL INFORMATION:
APPLICANT: Ryals, John A.
APPLICANT: Alexander, Danny C.
APPLICANT: Beck, James J.
APPLICANT: Duesling, John H.
APPLICANT: Friedrich, Leslie B.
APPLICANT: Goodman, Robert M.
APPLICANT: Harms, Christian
APPLICANT: Meins, Jr., Frederick
APPLICANT: Montoya, Alice
APPLICANT: Meyer, Mary B.
APPLICANT: Neuhaus, Jean-Harc
APPLICANT: Payne, George B.
APPLICANT: Sperison, Christoph
APPLICANT: Stinson, Jeffrey R.
APPLICANT: Uknes, Scott J.
APPLICANT: Ward, Eric R.
APPLICANT: Williams, Shericea C.
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
NUMBER OF INVENTION: DNA SEQUENCES AND USES THEREOF
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: CIBA-GEIGY Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: Hawthorne
COUNTRY: New York
ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/449,043
FILING DATE: 24-MAY-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/181,271
FILING DATE: 13-JAN-94
APPLICATION NUMBER: US 08/093,301

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; FILING DATE: 16-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/937,197
; FILING DATE: 6-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/678,378
; FILING DATE: 1-APR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/305,566
; FILING DATE: 6-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/165,667
; FILING DATE: 8-MAR-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/042,847
; FILING DATE: 6-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/632,441
; FILING DATE: 21-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/425,504
; FILING DATE: 20-OCT-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/848,506
; FILING DATE: 6-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/768,122
; FILING DATE: 27-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/580,431
; FILING DATE: 7-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/368,672
; FILING DATE: 20-JUN-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/329,018
; FILING DATE: 24-MAR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/045,957
; FILING DATE: 12-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Elmer, James Scott
; REGISTRATION NUMBER: 36,129
; REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8614
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 771 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-449-043-10

Alignment Scores:
Pred. No.: 3,12e-17
Score: 304.00
Percent Similarity: 56.55%
Best Local Similarity: 44.14%
Query Match: 28.02%
DB: 1 Gaps: 3

US-09-832-320-2 (1-203) x US-08-449-043-10 (1-771)
QY 61 SerGlySerAsnAlaThrAlaAspGluTyrLeuAlaProHisAsnGlnAlaArgAlaAla 80
Db 111 TCTCATGCCCAAACTCTCAACAAAGACTATTGGATGCCCATTAACACAGCTGTCAGAT 170
QY 81 ValGlyValAlaProLeuArgTrpAsnAlaGlyLeuAlaSerAlaAlaGlyThrVal 100
Db 171 GTAGGGCTGGACCATTAACCTGGACAAAGGGGTAGACCTATGACAAATAATGTT 230

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QY 101 Alaglnclnlarqarglnlglcysalaphnealaaspvalcylalaserytyrly 120
 Db 231 TCTCAATTGGCTGCAGACGCAACCTCGTACATTCAT-----GGCCAAATACGGC 281
 QY 121 Alaasn-----GlnGlyTTPAlaseryTfArqAlaArqProAlaGluValAlaAla 138
 Db 282 GAAACCTAGCTACAGGAAGTGGCGATTTATACG---GCTGCTAAGGCCGCTCGAGATG 338
 QY 139 TTPValAlaGlnGlyArqTfTfThrHisAlaAsnAsnThrcysAlaAlaGlyArqGln 158
 Db 339 TGGGTGATGAGAAACAGTACTATGACATGACTCAAAATCTGTGTCACAGACAGGTG 398
 QY 159 CysGlyThrTfThrGlnValAlaTTPArqAsnThrAlaGluValGlyCysAlaGlnAla 178
 Db 399 TGGGACACTATCTACGAGGTGGTGGCTAACCTGGTTCGTTGGATGTGTAGGGTT 458
 QY 179 SerCysAlaThrcGlyAlaThrLeuThrLeuThrcysLeuThrcysProHisGlyAsnValGln 198
 Db 459 AAGTGCACATGACAGATATGTGTCTCTTGCACACTATGATCTCCAGGTATGTGCATA 518
 QY 199 GlyGlnSerProTyr 203
 Db 519 GGCCAAAGTCCATAC 533

RESULT 6
 US-08-456-265A-10
 Sequence 10, Application US/08456265A
 Patent No. 5767369

GENERAL INFORMATION:

APPLICANT: Alexander, Danny C.
 APPLICANT: Ryals, John A.
 APPLICANT: Goodman, Robert M.
 APPLICANT: Stinson, Jeffrey R.
 TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
 TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
 NUMBER OF SEQUENCES: 111
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: CIBA-GEIGY Corporation
 STREET: 520 White Plains Road, P.O. Box 2005
 CITY: Tarrytown
 STATE: New York
 COUNTRY: USA
 ZIP: 10591

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/456,265A
 FILING DATE: 31-MAY-95
 CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/181,271
 FILING DATE: 13-JAN-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/093,301
 FILING DATE: 16-JUL-1993
 PRIOR APPLICATION DATA:

APPLICATION NUMBER:

APPLICATION NUMBER: US 07/937,197
 FILING DATE: 6-NOV-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/678,378
 FILING DATE: 1-APR-1991
 PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/305,566
 FILING DATE: 6-FEB-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/165,667
 FILING DATE: 8-MAR-1988
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/042,847

FILING DATE: 6-APR-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/632,441
 FILING DATE: 21-DEC-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/425,504
 FILING DATE: 20-OCT-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/848,506
 FILING DATE: 6-MAR-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/768,122
 FILING DATE: 27-SEP-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/580,431
 FILING DATE: 7-SEP-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/368,672
 FILING DATE: 20-JUN-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/329,018
 FILING DATE: 24-MAR-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/045,957
 FILING DATE: 12-APR-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Meigs, J. Timothy
 REGISTRATION NUMBER: 38,241
 REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727/DIV10
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (919)541-8587
 TELEFAX: (919)541-8689
 INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 771 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 US-08-456-265A-10

Alignment Scores:
 Pred. No.: 3.12e-17 Length: 771
 Score: 304.00 Matches: 64
 Percent Similarity: 56.55% Conservative: 18
 Best Local Similarity: 44.14% Mismatches: 57
 Query Match: 28.02% Indels: 6
 Gaps: 3

US-09-832-320-2 (1-203) x US-08-456-265A-10 (1-771)

QY 61 SerGlySerAsnAlaThrAlaAspGluTfThrLeuAlaProHisAsnGlnAlaArqAlaAla 80
 Db 111 TCTCATGCCCAAACTCTAACAAGACTTTTGATGCCATTAACAACGCTGTCAGAT 170
 QY 81 ValGlyValAlaProLeuArqTfThrHisAlaGlnGlyLeuAlaSerAlaAlaGlyThrVal 100
 Db 171 GTAGCGGTGAACATTACTTGGGACACGGGGTAGCAGCCTATGACCAAAATATATGTT 230
 QY 101 Alaglnclnlarqarglnlglcysalaphnealaaspvalcylalaserytyrly 120
 Db 231 TCTCAATTGGCTGCAGACGCAACCTCGTACATTCAT-----GGCCAAATACGGC 281
 QY 121 Alaasn-----GlnGlyTTPAlaseryTfArqAlaArqProAlaGluValAlaAla 138
 Db 282 GAAACCTAGCTACAGGAAGTGGCGATTTATACG---GCTGCTAAGGCCGCTCGAGATG 338
 QY 139 TTPValAlaGlnGlyArqTfTfThrHisAlaAsnAsnThrcysAlaAlaGlyArqGln 158
 Db 339 TGGGTGATGAGAAACAGTACTATGACATGACTCAAAATCTGTGTCACAGACAGGTG 398
 QY 159 CysGlyThrTfThrGlnValAlaTTPArqAsnThrAlaGluValGlyCysAlaGlnAla 178

DB 459 AAGTCACAAATGAGATATGTCTCTGCAACTATGATCTCCAGGATATGTCATA 518
OY 199 GYGLInserProTyr 203
DB 519 GGCACAAATGTCATAC 533

RESULT 8
US-08-455-244-10
; Sequence 10, Application US/08455244
; Patent No. 5789214

GENERAL INFORMATION:
APPLICANT: Ryals, John A.
APPLICANT: Alexander, Danny C.
APPLICANT: Beck, James J.
APPLICANT: Duesling, John H.
APPLICANT: Friedrich, Leslie B.
APPLICANT: Goodman, Robert M.
APPLICANT: Harms, Christian
APPLICANT: Melms, Jr., Frederick
APPLICANT: Montoya, Alice
APPLICANT: Moyer, Mary B.
APPLICANT: Neuhaus, Jean-Marc
APPLICANT: Payne, George B.
APPLICANT: Sperison, Christoph
APPLICANT: Stinson, Jeffrey R.
APPLICANT: Uknes, Scott J.
APPLICANT: Ward, Eric R.
APPLICANT: Williams, Shericka C.
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
NUMBER OF SEQUENCES: 106
TITLE OF SEQUENCES: DNA SEQUENCES AND USES THEREOF
CORRESPONDENCE ADDRESSES:
ADDRESSEE: CIBA-GEIGY Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: New York
COUNTRY: USA
ZIP: 10532

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,244
FILING DATE: 31-MAY-1995
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/181,271
FILING DATE: 13-JAN-94
APPLICATION NUMBER: US 08/093,301
FILING DATE: 16-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/937,197
FILING DATE: 6-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/678,378
FILING DATE: 1-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/305,566
FILING DATE: 6-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/165,667
FILING DATE: 8-MAR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/042,847
FILING DATE: 6-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/632,441
FILING DATE: 21-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/425,504

FILING DATE: 20-OCT-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/848,506
FILING DATE: 6-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/768,122
FILING DATE: 27-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/580,431
FILING DATE: 7-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/368,672
FILING DATE: 20-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/045,957
FILING DATE: 12-APR-1993
PRIOR APPLICATION DATA:
ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: S-19825/PI/CGC 1727
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8614
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 771 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-455-244-10

Alignment Scores:
Pred. No.: 3,12e-17 Length: 771
Score: 304.00 Matches: 64
Percent Similarity: 56.55% Conservative: 18
Best Local Similarity: 44.14% Mismatches: 57
Query Match: 28.02% Indels: 6
DB: 1 Gaps: 3

US-09-832-320-2 (1-203) x US-08-455-244-10 (1-771)

OY 61 SerGlySerAsnAlaThrAlaAspGluTyrLeuAlaProHisAsnGlnAlaArgAla 80
DB 111 TCTCATGGCCAAACCTCTCAACAAAGACTATTGGATGCCATACACAGCTCGTCAGAT 170
OY 81 ValGlyValAlaProLeuArgTyrAsnAlaGlyLeuAlaSerAlaAlaGlyTyrVal 100
DB 171 GTAGGGGTGGAACCATTTACTTTGGGACAAAGCGGTAGCAACCTATGCACAAATTATGTT 230
OY 101 AlAGlnGlnArgArgGlnGlnGlyCysAlaIleAlaAspValGlyAlaSerProTyrGly 120
DB 231 TCTCAATTGGCTGACAGACTGCAACCTCGTACATCTCAT-----GCCCAATACGGC 281
OY 121 AlaAsn-----GlnGlyTyrPalaSerTyrArgAlaArgProAlaGlnValAlaLeu 138
DB 282 GAACCTAGCTAGGAGGAGTGGCGATTTTATGACG---GCTGTAAGCCGTCGAGTGT 338
OY 139 TrpValAlaGlnGlyArgTyrTyrThrHisAlaAsnAsnThrCysAlaAlaGlyArgGln 158
DB 339 TGGGTGATGAACAAACAGTACTATGACCTGACCTAAATACTGTGTGCACAAAGACAGTG 398
OY 159 CysGlyThrTyrThrGlnValValTyrPargAsnThrAlaGlnValGlyCysAlaGlnAla 178
DB 399 TGTGACACTATACCTAGGTGTGGGTGCGTACCTCGGTGCGTGTGATGTCTAGGCTT 458
OY 179 SerCysAlaThrGlyAlaThrLeuThrLeuCysLeuTyrAsnProHisGlyAsnValGln 198
DB 459 AAGTCACAAATGAGATATGTGTCTCTGCAACTATGATCTCCAGGATATGTCATA 518

QY 199 GlynSerProtyr 203
DB 519 GGCCAAAGTCATAC 533

RESULT 9

US-08-454-876-10
Sequence 10, Application US/08454876

Patent No. 5804693

GENERAL INFORMATION:

APPLICANT: Ryals, John A.
APPLICANT: Alexander, Danny C.
APPLICANT: Beck, James J.
APPLICANT: Duesling, John H.
APPLICANT: Friedlich, Leslie B.
APPLICANT: Goodman, Robert M.
APPLICANT: Harms, Christian
APPLICANT: Meins, Jr., Frederick
APPLICANT: Montoya, Alice
APPLICANT: Moyer, Mary B.
APPLICANT: Neuhaus, Jean-Marc
APPLICANT: Payne, George B.
APPLICANT: Sperison, Christoph
APPLICANT: Stinson, Jeffrey R.
APPLICANT: Uknes, Scott J.
APPLICANT: Ward, Eric R.
APPLICANT: Williams, Shericea C.
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: CIBA-GEIGY Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: New York
COUNTRY: USA
ZIP: 10532

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/454,876

FILING DATE: 31-MAY-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/181,271

FILING DATE: 13-JAN-94

APPLICATION NUMBER: US 08/093,301

FILING DATE: 16-JUL-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/937,197

FILING DATE: 6-NOV-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/678,378

FILING DATE: 1-APR-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/305,566

FILING DATE: 6-FEB-1989

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/165,667

FILING DATE: 8-MAR-1988

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/042,847

FILING DATE: 6-APR-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/632,441

FILING DATE: 21-DEC-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/425,504

FILING DATE: 20-OCT 1989

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/848,506

FILING DATE: 6-MAR-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/768,122

FILING DATE: 27-SEP-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/580,431

FILING DATE: 7-SEP-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/368,672

FILING DATE: 20-JUN-1989

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/329,018

FILING DATE: 24-MAR-1989

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/045,957

FILING DATE: 12-APR-1993

ATTORNEY/AGENT INFORMATION:

NAME: Elmet, James Scott

REGISTRATION NUMBER: 36,129

REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727

TELECOMMUNICATION INFORMATION:

TELEPHONE: (919)541-8614

TELEFAX: (919)541-8689

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 771 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: CDNA

US-08-454-876-10

Alignment Scores:

Pred. No.: 3,12e-17 Length: 771

Score: 304.00 Matches: 64

Percent Similarity: 56.55% Conservative: 18

Best Local Similarity: 44.14% Mismatches: 57

Query Match: 28.02% Indels: 6

DB: 1 Gaps: 3

US-09-832-320-2 (1-203) x US-08-454-876-10 (1-771)

QY 61 SerGlySerAsnAlaThrAlaAspLunrYrLeuAlaProHisAsnGlnAlaArgAla 80
DB 111 TCTCATGCCCAAACTCTCAACAGACTATTGGATGCCCTTAACAGCTGTCAGAT 170
QY 81 ValGlyValAlaProLeuArgTyrPanaAlaGlyLeuAlaSerAlaAlaGlyThrVal 100
DB 171 GTAGCGGTGGAACCACTTAAGTGGGCAACCGGTAGACGCTATGCACAAATATATGT 230
QY 101 AlAGlGlnAlaArgGlnGlnGlyCysAlaPheAlaAspValGlyAlaSerProTyrGly 120
DB 231 TCTCATGTGGTCGACAGCTGCAACTGCTACATCTCAT-----GGCAATACGGC 281
QY 121 AlaAsn-----GlnGlyTyrPalasertYrAlaArgAlaArgProAlaGlnValAlaLeu 138
DB 282 GAAGACCTACCTCAGGAGGTGGCGATTATTATGCG--GCTGTAAGGCGCGAGAG 338
QY 139 TrpValAlaGlnGlyArgTyrTyrThrHisAlaAsnAsnThrCysAlaAlaGlnArgGln 158
DB 339 TGGGTGATGAGAAACAGACTATGACCATGACATCAATCTTGTGCACAGACAGCGTG 398
QY 159 CysGlyThrTyrThrGlnValValTrpArgAsnThrAlaGlnValGlyCysAlaGlnAla 178
DB 399 TGTGACACTATACCTCAGGTGGTGGCTAGCTCGCTGCTGATGATGCTAGCGTT 458
QY 179 SerCysAlaThrGlyAlaThrLeuThrLeuCysLeuTyrAsnProHisGlnAsnValGln 198
DB 459 AAGTCAACAATGAGAGATATGTGTCTTGCACACTATGATCTCCAGGATATGTCCATA 518
QY 199 GlynSerProtyr 203
DB 519 GGCCAAAGTCATAC 533


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: Sequence 10, Application US/08456262
: Patent No. 5851766
: GENERAL INFORMATION:
: APPLICANT: Kyalis, John A.
: APPLICANT: Alexander, Danny C.
: APPLICANT: Beck, James J.
: APPLICANT: Duesing, John H.
: APPLICANT: Friedrich, Leslie B.
: APPLICANT: Goodman, Robert M.
: APPLICANT: Harms, Christian
: APPLICANT: Helms, J., Frederick
: APPLICANT: Montoya, Alice
: APPLICANT: Moyer, Mary B.
: APPLICANT: Neuhaus, Jean-Marc
: APPLICANT: Payne, George B.
: APPLICANT: Sperison, Christoph
: APPLICANT: Stinson, Jeffrey R.
: APPLICANT: Uthne, Scott J.
: APPLICANT: Ward, Eric R.
: TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
: TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
: NUMBER OF SEQUENCES: 106
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: CIBA-GEIGY Corporation
: STREET: 7 Skyline Drive
: CITY: Hawthorne
: STATE: New York
: COUNTRY: USA
: ZIP: 10532
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/456,262
: FILING DATE: 31-MAY-1995
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/181,271
: FILING DATE: 13-JAN-94
: APPLICATION NUMBER: US 08/093,301
: FILING DATE: 16-JUL-1993
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/937,197
: FILING DATE: 6-NOV-1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/678,378
: FILING DATE: 1-APR-1991
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/305,566
: FILING DATE: 6-FEB-1989
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/165,667
: FILING DATE: 8-MAR-1988
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/042,847
: FILING DATE: 6-APR-1993
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/632,441
: FILING DATE: 21-DEC-1990
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/425,504
: FILING DATE: 20-OCT-1989
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/848,506
: FILING DATE: 6-MAR-1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/768,122
: FILING DATE: 27-SEP-1991
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/580,431

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: FILING DATE: 7-SEP-1990
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/368,672
: FILING DATE: 20-JUN-1989
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/329,018
: FILING DATE: 24-MAR-1989
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/045,957
: FILING DATE: 12-APR-1993
: ATTORNEY/AGENT INFORMATION:
: NAME: Elmer, James Scott
: REGISTRATION NUMBER: 36,129
: REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (919)541-8614
: TELEFAX: (919)541-8689
: INFORMATION FOR SEQ ID NO: 10:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 771 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: US-08-456-262-10

Alignment Scores:
Pred. No.: 3 12e-17 Length: 771
Score: 304.00 Matches: 64
Percent Similarity: 56.35% Conservative: 18
Best Local Similarity: 44.14% Mismatches: 57
Query Match: 28.02% Indels: 6
DB: Gaps: 3

US-09-832-320-2 (1-203) x US-08-456-262-10 (1-771)
QY 61 SerGlySerAsnAlaThrAlaAspGluTyrLeuAlaProHisAsnGlnAlaArgAlaAla 80
   |||  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::
Db 111 TCTCATGCCCCAAACCTCCACACAGACTATTTGGATGCGCATTAACACAGCTCGCAGCAT 170
QY 81 ValGlyValAlaProLeuArgTyrPAsnAlaGlyLeuAlaSerAlaAlaAlaGlyThrVal 100
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 171 GTAGGCGTGAACCATTAATTACTGGGCAACGGGGTAGCAGCCATGCAACAATTTAGTT 230
QY 101 AlaGlnGlnArgArgGlnGlnGlyGlyCysAlaIleAlaAspValGlyAlaSerProTyrGly 120
   ::|||  ::|||  ::|||  ::|||  ::|||  ::|||  ::|||  ::|||  ::|||  ::|||
Db 231 TCTCAATGGCTGCAGACTGCACAACCTGTAATTCAT-----GGCCAATACGGC 281
QY 121 AlaAsn-----GlnGlyTyrPAlaSerTyrArgAlaArgProAlaGluValAlaAlaLeu 138
   |||  |||  |||  |||  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::
Db 282 GAAACCTAGCTCAGGGAAGTGGCGATTTTATGACG--GCTGCTAAGCGCGTCGAGATG 338
QY 139 TrpValAlaGlnGlyArgTyrTyrThrHisAlaAsnAsnThrCysAlaAlaGlyArgGln 158
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Db 339 TGGGTGATGAGAAACAGTACTGACATGACATGACATGACATGACATGACATGACATG 398
QY 159 CysGlyThrTyrThrGlnValAlaTyrPArgAsnThrAlaGluValGlyCysAlaGlnAla 178
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QY 179 SerCysAlaThrGlyAlaThrLeuThrLeuCysLeuTyrAsnProHisGlyAsnValGln 198
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QY 199 GlyGlnSerProTyr 203
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RESULT 12
US-08-456-240-10
: Sequence 10, Application US/08456240
: Patent No. 585154
: GENERAL INFORMATION:

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      FILING DATE: 20-JUN-1989
      PRIOR APPLICATION DATA:
      APPLICATION NUMBER: US 07/329,018
      FILING DATE: 24-MAR-1989
      PRIOR APPLICATION DATA:
      APPLICATION NUMBER: US 08/045,957
      FILING DATE: 12-APR-1993
      ATTORNEY/AGENT INFORMATION:
      NAME: Elmer, James Scott
      REGISTRATION NUMBER: 36,129
      REFERENCE/DOCKET NUMBER: S-19825/PI/CGC 1727
      TELECOMMUNICATION INFORMATION:
      TELEPHONE: (919)541-8614
      TELEFAX: (919)541-8689
      INFORMATION FOR SEQ ID NO: 10:
      SEQUENCE CHARACTERISTICS:
      LENGTH: 771 base pairs
      TYPE: nucleic acid
      STRANDEDNESS: single
      TOPOLOGY: linear
      MOLECULE TYPE: cDNA
      US-08-456-240-10

Alignment Scores:
Pred. No.: 3,12e-17 Length: 771
Score: 304.00 Matches: 64
Percent Similarity: 56.55% Conservative: 18
Best Local Similarity: 44.14% Mismatches: 57
Query Match: 28.02% Indels: 6
                Gaps: 3

US-09-832-320-2 (1-203) x US-08-456-240-10 (1-771)

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QY      81  Valglvvalalaprroleuargtrpshnrlgilyleualaserlalalagllyhrval 100
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Db      171  GRAGCGGTGGAGAACCATTAATCTTGGGACCAAGGGGTGGACGCTTGTGCAAAATTTATGT 230

QY      101  Alaglnglnargrarglngllyglcysnlaphealaserpvalglvalaserprotyrgly 120
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Db      231  TCTCAATTGGCTGCAACACGCAACCTCGTACATTCAT-----GGCCAAATAGGCG 281

QY      121  Alaaan-----Glnglytrpalseertryrgralargproalaglvalalaleu 138
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Db      282  GAAACCTAGTCACGGGAAGTGGCGATTTTATAGC---GCTGCTAAGGCCGTCAGATG 338

QY      139  Trpvallalaglunlgrtyrtyrthnlalslasnshnrhrcysalaaaglyargln 156
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QY      159  Cysglythrtyrthrlnvalvaltrpargasnthralagluvalglcysalaglinala 178
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Db      399  TGTGGACACTATACCTGAGGTGTGGGTGGGTGATCTCGTGTGGATGTGCTAGGGTT 458

QY      179  SerCysalathrthrlyalahrthleuhsyleuetyyaanprohsaglvalnlgln 196
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QY      199  GlylglnserProtyr 203
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Db      519  GCCCAAACTCCATAC 533

RESULT 13
US-08-455-736-10
: Sequence 10 Application US/08455736
: Patent No. 5880328
: GENERAL INFORMATION:
: APPLICANT: Ryals, John A.
: APPLICANT: Alexander, Danny C.
: APPLICANT: Beck, James J.

```

APPLICANT: Duesing, John H.
APPLICANT: Friedlich, Leslie B.
APPLICANT: Goodman, Robert M.
APPLICANT: Harms, Christian
APPLICANT: Meins, Jr., Frederick
APPLICANT: Montoya, Alice
APPLICANT: Moyer, Mary B.
APPLICANT: Neuhaus, Jean-Marc
APPLICANT: Payne, George B.
APPLICANT: Sperison, Christopher
APPLICANT: Stinson, Jeffrey R.
APPLICANT: Uknes, Scott J.
APPLICANT: Ward, Eric R.
APPLICANT: Williams, Shericea C.
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: CIBA-GEIGY Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: New York
COUNTRY: USA
ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 08/455,736
FILING DATE: 31-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/181,271
FILING DATE: 13-JAN-1994
APPLICATION NUMBER: US 08/093,301
FILING DATE: 16-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/937,197
FILING DATE: 6-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/678,378
FILING DATE: 1-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/305,566
FILING DATE: 6-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/165,667
FILING DATE: 8-MAR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/042,847
FILING DATE: 6-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/632,441
FILING DATE: 21-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/425,504
FILING DATE: 20-OCT-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/848,506
FILING DATE: 6-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/768,122
FILING DATE: 27-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/580,431
FILING DATE: 7-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/368,672
FILING DATE: 20-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/329,018

FILING DATE: 24-MAR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/045,957
FILING DATE: 12-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Elmer James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8614
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 771 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-455-736-10
Alignment Scores:
Pred. No.: 3,12e-17 Length: 771
Score: 304.00 Matches: 64
Percent Similarity: 56.55% Conservative: 18
Best Local Similarity: 44.14% Mismatches: 57
Query Match: 28.02% Indels: 6
Gaps: 3
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QY 61 SerGlySerAsnAlaThrAlaAspGluTyrLeuAlaProHisAsnGlnAlaArgAlaAla 80
Db 111 TCTCATGCCCAAACTCTCAACAGACTATTGGATGCCCAACAGCTCTGCACAT 170
QY 81 ValGlyValAlaProLeuArgTrpAsnAlaGlyLeuAlaSerAlaAlaAlaGlyThrVal 100
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QY 121 AlaAsn-----GlnGlyTrpAlaSerTyrArgAlaArgProAlaGlnValValAlaLeu 138
Db 282 GAATACCTAGCTCAGGAGAGTGGCGATTATGACG---GCTGCTAAGCGCTGCAGATG 338
QY 139 TrpValAlaGlnGlyArgTyrTyrHisAlaAsnAsnThrCysAlaAlaGlyArgGln 158
Db 339 TCGCTGCATGAGAAACAGTACTATGACACATGACTCAATATCTGTGCACAGACAGGTG 398
QY 159 CysGlyThrTyrTrpGlnValAlaTrpArgAsnThrAlaGlnValGlyCysAlaGlnAla 178
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QY 179 SerCysAlaThrGlyAlaThrLeuThrLeuCysLeuTyrAsnProHisGlyAsnValGln 198
Db 459 AAGTCAACAATGAGAGATATGTTGCTGTGCACACTATGATCCACGTAATGTCAATA 518
QY 199 GlyGlnSerProTyr 203
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RESULT 14
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Sequence 10, Application us/08971217
Patent No. 5942662
GENERAL INFORMATION:
APPLICANT: Ryals, John A.
APPLICANT: Harms, Christian
APPLICANT: Friedlich, Leslie
APPLICANT: Beck, James
APPLICANT: Uknes, Scott
APPLICANT: Ward, Eric

MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/350,600
 FILING DATE:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/971,217
 FILING DATE: 14-NOV-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/457,364
 FILING DATE: 31-MAY-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/181,271
 FILING DATE: 13-JAN-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/093,301
 FILING DATE: 16-JUL-1993
 PRIOR APPLICATION DATA:
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 FILING DATE: 21-DEC-1990
 PRIOR APPLICATION DATA:
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 APPLICATION NUMBER: US 07/848,506
 FILING DATE: 6-MAR-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/768,122
 FILING DATE: 27-SEP-1991
 PRIOR APPLICATION DATA:
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 PRIOR APPLICATION DATA:
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 FILING DATE: 18-JUL-1989
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 APPLICATION NUMBER: US 07/353,312
 FILING DATE: 17-MAY-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/226,303
 FILING DATE: 29-JUL-1988
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/045,957
 FILING DATE: 12-APR-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Meigs, J. Timothy
 REGISTRATION NUMBER: 38,241
 REFERENCE/DOCKET NUMBER: S-198250
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (919)541-8587

TELEFAX: (919)541-8689
 INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 771 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 US-09-350-600-10
 Alignment Scores:
 Pred. No.: 3,12e-17 Length: 771
 Score: 304.00 Matches: 64
 Percent Similarity: 56.55% Conservative: 18
 Best Local Similarity: 44.14% Mismatches: 57
 Query Match: 28.02% Indels: 6
 Gaps: 3
 DB:
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GenCore version 5.1.4.P5.A578
Copyright (c) 1993 - 2003 CompuGen Ltd.

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Database: Published Applications.NA.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	333	30.7	749	10	US-09-840-479-12
4	300.5	27.7	772	9	US-10-068-347-3

5	297.5	27.4	492	9	US-09-938-842A-1676	Sequence 1676, Ap
6	294	27.1	501	9	US-09-938-842A-2002	Sequence 2002, Ap
7	292.5	27.0	866	10	US-09-840-479-6	Sequence 6, Appl1
8	288	26.5	486	10	US-09-938-842A-2047	Sequence 2047, Ap
9	288	26.5	738	9	US-09-887-576-608	Sequence 608, App
10	288	26.5	757	10	US-09-887-576-618	Sequence 618, App
11	287	26.5	714	12	US-10-078-929-85	Sequence 85, Appl
12	280.5	25.9	604	12	US-10-078-929-99	Sequence 99, Appl
13	264	24.3	783	12	US-10-078-929-81	Sequence 81, Appl
14	264	24.3	806	10	US-09-840-479-14	Sequence 14, Appl
15	255	23.5	701	12	US-10-078-929-95	Sequence 95, Appl
16	254	23.4	939	12	US-10-078-929-89	Sequence 89, Appl
17	249	22.9	547	12	US-10-078-929-97	Sequence 97, Appl
18	248	22.9	718	12	US-10-078-929-93	Sequence 93, Appl
19	236	21.8	534	12	US-10-078-929-83	Sequence 83, Appl
20	231	21.3	664	9	US-10-068-347-1	Sequence 1, Appl1
21	223.5	20.6	525	9	US-10-068-347-9	Sequence 9, Appl1
22	205	18.9	1876	9	US-09-944-413-49	Sequence 49, Appl
23	205	18.9	1876	9	US-09-944-403-49	Sequence 49, Appl
24	205	18.9	1876	9	US-09-944-896-49	Sequence 49, Appl
25	205	18.9	1876	9	US-09-944-944-49	Sequence 49, Appl
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35	205	18.9	1876	10	US-09-944-332-49	Sequence 49, Appl
36	205	18.9	1876	10	US-09-943-762-49	Sequence 49, Appl
37	205	18.9	1876	10	US-09-943-654-49	Sequence 49, Appl
38	205	18.9	1876	10	US-09-943-851A-49	Sequence 49, Appl
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42	200	18.4	1923	9	US-10-042-141-12	Sequence 12, Appl
43	200	18.4	1923	10	US-09-726-643-12	Sequence 12, Appl
44	197	18.2	483	9	US-09-938-842A-1683	Sequence 1683, Ap
45	196	18.1	472	12	US-10-078-929-91	Sequence 91, Appl

ALIGNMENTS

RESULT 1
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Sequence 3, Application US/09832320
Patent NO. US20010049834A1
GENERAL INFORMATION:
APPLICANT: Crane, Edmund H.
TITLE OF INVENTION: Maltz pathogenesis-Related
TITLE REFERENCE: 35718/214291
CURRENT APPLICATION NUMBER: US/09/832,320
CURRENT FILING DATE: 2001-04-10
PRIOR APPLICATION NUMBER: US 60/195,801
PRIOR FILING DATE: 2000-04-10
NUMBER OF SEQ ID NOS: 3
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 612
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(612)
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Alignment Scores:

Pred. No.:

Percent Similarity

Best Local Similarity
Query Match:
DB:

US-09-832-320-2 (1-203) x US-09-832-320-1 (1-898),

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Oy      21 CysLeuLeuLeuAlaThrLeuLeuAlaLeuCysAlaAlaProAlaProHisGlyAla 40
        |||
Db      123 TGGCTTCCTCCGCGCACCTCTCCGCTGTGGCGCGCGCGCGCGCACCGAGCGCG 182
Oy      41 ArgValLeuMetProGlyGlyAlaGlyAlaValThrTysAlaGlnGlnGlyTyrHisGly 60
        |||
Db      183 CGGCTCCATACCGAGGGGGGGGGGGGGGGGGGGTGAACAGGCGAGAGGGGTGGACGGC 242
Oy      61 SerGlySerAsnAlaThrAlaAspGluTyrLeuAlaProHisAsnGlnAlaArgAlaAla 80
        |||
Db      243 AGCGGCGAGCAAGCGCGAGCGGAGAGACTGGCGCGCCGACAAACGAGCGCGCGCGCG 302
Oy      81 ValGlyValAlaProLeuArgTyrPheAsnGlyLeuAlaSerAlaAlaGlyTyrVal 100
        |||
Db      303 GTGGGGGTGGCCCGCTGGGGGGGAACCGGGCTGGCTTGGCGCGCGCGGGAGCGGTG 362
Oy      101 AlaGlnGlnArgArgGlnGlyGlyCysAlaPheAlaAspValGlyAlaSerProTyrGly 120
        |||
Db      363 GCCACAGAGCGGCGAGGGGGGGGGCGCGCTCCGCGAGCTGGGGCGCACGCCCTACGCG 422
Oy      121 AlaAsnGlnGlyTyrAlaSerTyrPheAlaArgProAlaGlnValValAlaLeuThrPheAl 140
        |||
Db      423 GCGAACCAAGGGGTGGCGAGCTACCGCGCGCGCGCGCGCGCGAGGTGGCTGTGGGTG 482
Oy      141 AlaGlnGlyArgTyrTyrThrHisAlaAsnAsnThrCysAlaAlaGlyArgGlnCysGly 160
        |||
Db      483 GCGAGGGGGGGGTACTACACCGACCAACACAGTGGCGCGCGGGCGGCGAGTGGCGC 542
Oy      161 ThrTyrThrGlnValValTyrPheArgSerPheAlaGlnValGlyCysAlaGlnAlaSerCys 180
        |||
Db      543 ACGTACACGAGGTGGTGTGGGGCAACCGCGCGAGGTGGGGTGGCGGAGGCCAGCTGC 602
Oy      181 AlaThrGlyAlaThrLeuThrLeuCysLeuTyrAsnProHisGlyAsnValGlnGln 200
        |||
Db      603 GCCACGGCGCGCCACGCTCAGCTGTGCTGTACAAACCGGACGCGCAAGTGAAGGGCAG 662
Oy      201 SerProTyr 203
        |||
Db      663 AGCCCTTAC 671

RESULT 3
US-09-840-479-12
: Sequence 12, Application us/09840479
: Patent No. US20010025380A1
: GENERAL INFORMATION:
: APPLICANT: Crane, Virginia
: TITLE OF INVENTION: Family Of Maize PR-1 Genes And Promoters
: FILE REFERENCE: 5718-32, 035718/175219
: CURRENT APPLICATION NUMBER: US/09/840,479
: CURRENT FILING DATE: 2001-04-23
: PRIORITY APPLICATION NUMBER: 09/257,583
: PRIORITY FILING DATE: 1999-02-25
: NUMBER OF SEQ ID NOS: 37
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 12
: LENGTH: 749

```

[illegible]

```

: CURRENT FILING DATE: 2002-02-06
: PRIOR APPLICATION NUMBER: 60/267,052
: PRIOR FILING DATE: 2001-02-07
: NUMBER OF SEQ ID NOS: 12
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 3
: LENGTH: 772
: TYPE: DNA
: ORGANISM: Zea mays
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (56)..(571)
US-10-068-347-3

Alignment Scores:
Pred. No.: 2.07e-18 Length: 772
Score: 300.50 Matches: 70
Percent Similarity: 52.10% Conservative: 17
Best Local Similarity: 41.92% Mismatches: 63
Query Match: 27.70% Indels: 17
DB: 9 Gaps: 7

US-09-832-320-2 (1-203) x US-10-068-347-3 (1-772)
QY 42 ValLeuMetProGlyValAlaGlyAlaValAlaThrLysAlaGlnGlnGlyValGlyThrGlySer 61
   |||||
Db 104 GNGGGGGCGCGCGCGCGCTGCGCGCTGCTGCTGCGGCCAAGC----- 148
QY 62 GlySerAsnAlaThrAlaAspGluThrLeuAlaProHisAsnGlnAlaArgAlaAlaVal 81
   |||||
Db 149 -----ACGGCGCGAGCACTTCGTGAACCTGCACAACTCCCGCGCGGAGCG 196
QY 82 GlyValAlaProLeuArgThrAsnAlaGlyLeuAlaSerAlaAlaAlaGlyThrValAla 101
   |||||
Db 197 GCGCGTCGGGAACGTGCGCTGGAAACACACAGGTGGCG--GCGTACGGCGAGGCTACGCG 253
QY 102 GlnGlnArgArgGlnGlyValGlyCysAlaPheAlaAspValGlyAlaSerProTyrGlyAla 121
   |||||
Db 254 AACCAAG---CGCGCGGCGACTGCGCGGTGTGCACCTCGCG--GGGCGCTACGGGGAG 307
QY 122 AsnGlnGlyTrp-----AlaSerTyrArgAlaArgProAlaGlnValAlaAlaLeuTrp 139
   |||||
Db 308 AACCTGCTCTGGGCGCTCGCGGCGCTACCGCTGAGCGGCGTCCAGCCGCTGGGATCTCG 367
QY 140 ValAlaGlnGlyArgTyrTyrThrHisAlaAsnAsnThrCysAlaAla-----GlyArg 157
   |||||
Db 368 GCGGCGGAGAACACTACTACCAACGCGCACCACTGCTCGGCTCCGTCGGCGGCCAG 427
QY 158 GlnCysGlyThrTyrThrGlnValValTrpArgAsnThrAlaGlnValGlyCysAlaGln 177
   |||||
Db 428 TCGTCGCGCACTACACGACGTGTGTGGCGCGCTCCACTCGCATGCGATGCGCCCGC 487
QY 178 AlaSerCysAlaThrGlyAla---ThrLeuThrLeuGlyCysLeuTyrAsnProHisGln 196
   |||||
Db 488 GTCGCTGCAGCAACAACGCGCGCTTTCATCATCTGCACTATTACCGCGCGGCAAC 547
QY 197 ValGlnGlyGlnSerProTyr 203
   |||||
Db 548 GTGATTGGACAGAGCCCTTAC 568

RESULT 5
US-09-938-842A-1676
: Sequence 1676, Application US/09938842A
: Patent No. US20020160378A1
: GENERAL INFORMATION:
: APPLICANT: Harper, Jeff
: APPLICANT: Kreps, Joel
: APPLICANT: Wang, Xun
: APPLICANT: Zhu, Tong
: TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
: FILE REFERENCE: SRIPI300-3
: CURRENT APPLICATION NUMBER: US/09/938, 842A

```

```

; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO: 1676
; LENGTH: 492
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; US-09-938-842A-1676

```

Alignment Scores:

```

Pred. No.: 2,21e-18 Length: 492
Score: 297.50 Matches: 61
Percent Similarity: 57.78% Conservative: 17
Best Local Similarity: 45.19% Mismatches: 34
Query Match: 27.42% Indels: 3
DB: Gaps: 2

```

US-09-832-320-2 (1-203) x US-09-938-842A-1676 (1-492)

```

QY 69 GUTYRLLEUAlARPROHIAASNGIALAAGAlAAlAValGlyAlAAlAProLeuAlaArgTyr 88
DB 94 GACTTTTGGCGATTCCACACCGAGCCGAGGTGGGGGACCCCTTAAGATGG 153
QY 89 ASNAIAGIYLEUAlASerAlAAlAAGIYThrValAlAGInGInARgARgInGly 108
DB 154 GAGGAGAAGGTGGCTTATGCGGTATGCTAACAG-----CGTAAAGGTGAC 207
QY 109 CYSAlARPhEAlAASpValGlyAlASerProtyrGlyAlAAsnGInGlyTyrAlASerTyr 128
DB 208 TCGGCTATGAAACACTCGACGGGCTC---TATGAGAGAAACATCGCTTGGACACGGCT 264
QY 129 ACPAlAARProAlAGIYAlAAlAAlAAlAAlAAlAAlAAlAAlAAlAAlAAlAAlA 148
DB 265 ACCATGACGCGGTGACGACGAGTTCACATGTCGGTGGCGACGAATTGACATGATTA 324
QY 149 AAlAAsnARPhrCYAlAAlAAlAGIYArgGInGlyThrThrGInValAlATPArg 168
DB 325 GATTCCTAATACATGTGCTATGGACAAACAGTGTGCCACTATGCTGGTGTGGAGA 384
QY 169 ASnThrAlAGIYAlAGIYCYAlAGInAlASerCYAlAAlAAlAAlAAlAAlAAlA 188
DB 385 AACTGGAGAGGTGGGATGTGCAAAAGTGAAGATGCAACAATGGTCAACCTTATACAT 444
QY 189 CYSLEuTYRAsnPROHISGlyASnValGInGlyGInSerProtyr 203
DB 445 TGCACATACGATCTCCCGGTAACTGGGTGGCGAGTGGCCCTTAC 489

```

RESULT 6
US-09-938-842A-2002
; Sequence 2002, Application US/09938842A
; Patent No. US20020160378A1

```

; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE REFERENCE: SCRIPT300-3
; CURRENT APPLICATION NUMBER: US/09/938, 842A
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379

```

```

; SEQ ID NO 2002
; LENGTH: 501
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; US-09-938-842A-2002

```

Alignment Scores:

```

Pred. No.: 4.61e-18 Length: 501
Score: 294.00 Matches: 70
Percent Similarity: 47.09% Conservative: 19
Best Local Similarity: 37.04% Mismatches: 72
Query Match: 27.10% Indels: 28
DB: Gaps: 4

```

US-09-832-320-2 (1-203) x US-09-938-842A-2002 (1-501)

```

QY 15 AlARProMetAlARPhrAlACysLeuAlAAlAAlAAlAAlAAlAAlAAlAAlAAlA 34
DB 16 TCTCTCAAAACCTTACTACTATGCGATTAGCTCTTGTCTCACTTT---GCAAGTCCA 72
QY 35 AlARProThrISGLYAlAARgYAlLeuMetProGlyAlAGIYAlAAlAAlAAlAAlA 54
DB 73 -----CTGAAGACC 81
QY 55 GInGInGlyGlyThrGlySerGlySerAlAAlAAlAAlAAlAAlAAlAAlAAlAAlA 74
DB 82 CAAAGAC-----CGCGCAAGAGCTACTCTGATGTACAC 114
QY 75 ASnGInAlAARgAlAAlAAlAAlAGIYAlAAlAAlAAlAAlAAlAAlAAlAAlAAlA 94
DB 115 AACCATCTCGACGACGAGCTAGTACTGCTCATATTAATAATGACATCGGGA---GCAACC 171
QY 95 AlAAlAAlAAlAAlAAlAAlAAlAGInGInARgARgInGlyCYAlARPhEAlAASpVal 114
DB 172 CGATACCCCTGGAACTATGCTCAAGAGAAAGAGCGGAGCTGCTGCTCATCTCAAC 231
QY 115 GYAlASerProtyrGlyAlAAlAAlAGInGlyTyrAlAAlAAlAAlAAlAAlAAlA 134
DB 232 TCACGCGGAGCTTACAGGTGAACCTTGGCATGAGAGAGTGCATATGCCGAGCTGCC 291
QY 135 ValValAlAAlAAlAAlAAlAAlAGIYArgGInGlyThrThrGInValAlATPArg 154
DB 292 GCACTAGATGTGGGTGACGAGAAAGTCTGACTACTTCCAAATAACATACATCCGT 351
QY 155 AlAGIYArgGInGlyThrThrGInValAlATPArgAsnThrAlAGIYAlAGIY 174
DB 352 GCTGGAACAAACATGCTATATCTCAAGTGTGGAAACCTCAAGAGTGGTGA 411
QY 175 CYSAlAAlAAlASerCYAlAAlAAlAAlAAlAAlAAlAAlAAlAAlAAlAAlAAlA 194
DB 412 TGTGCCAAAGTCAAGTGTGCAATGGTGAACCTTGTGACTTGTCACTATTCATCT 471
QY 195 GYASnValGInGlyGInSerProtyr 203
DB 472 GGTATGTAGGGAGCTAGCCCTTAC 498

```

RESULT 7

```

US-09-840-479-6
; Sequence 6, Application US/09840479
; Patent No. US20010025380A1
; GENERAL INFORMATION:
; APPLICANT: Crane, Virginia
; TITLE OF INVENTION: Family of Maize PR-1 Genes and Promoters
; FILE REFERENCE: 5718-32, 035718/175219
; CURRENT APPLICATION NUMBER: US/09/840,479
; PRIOR FILING DATE: 2001-04-23
; PRIOR APPLICATION NUMBER: 09/257,583
; PRIOR FILING DATE: 1999-02-25
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 866
; TYPE: DNA

```

ORGANISM: Zea mays
FEATURE:
NAME/KEY: CDS
LOCATION: (111)..(581)
US-09-840-479-6

Alignment Scores:
Pred. No.: 1,21e-17 Length: 866
Score: 292.50 Matches: 74
Percent Similarity: 51.87% Conservative: 23
Best Local Similarity: 39.57% Mismatches: 57
Query Match: 26.96% Indels: 34
DB: 10 Gaps: 8

US-09-832-320-2 (1-203) x US-09-840-479-6 (1-866)

```

QY 21 CysteuleuAlaThrLeuAlaLeuCysAlaAlaProAlaProThrHisGlyAla 40
DB 90 TGTTCAGCTGCGCG-----TTGGCCATGCTCCG----- 119
QY 41 ArgValLeuMetProGlyGlyAlaGlyAlaValThrLysAlaGlnGlnGlyThreGly 60
DB 120 -----GTGATGCCGTGCGCG----- 137
QY 61 SerGlySerAsnAlaThrAlaAspGluTyrLeuAlaProHisAsnGlnAlaArgAlaAla 80
DB 138 -----CAGAACCTGCGCGCAGAAC---TTGCTGAACCCGACACATGCGCGCGCGCGCC 188
QY 81 ValGlyValAlaProLeuAlaGlyTyrPheAlaGlyLeuAlaSerAlaAlaAlaGlyThyVal 100
DB 189 GTGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 248
QY 101 AlaGlnAlaArgAlaGlnGlyGlyCysAlaPheAlaAspValGlyAlaSerPro----- 118
DB 249 GCGCAG-----CGCCAGGGGCGACTGCAACCTGCTCCGCGCGCGCGCGCGCGCGCGCGCG 302
QY 119 TyrGlyAlaAsnGlnGlyTyrAlaSerTyrArgAla---ArgProAlaGlnValValAla 137
DB 303 TACGGGAGAACCTTCTGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 362
QY 138 LeuTyrPheAlaGlnGlyArgTyrTyrHisAlaAsnThrCysAlaAlaGlyArg 157
DB 363 TTGTGGTGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 422
QY 158 GlnCysGlyTyrTyrThrGlnValAlaThrPheAsnThrAlaGlnValGlyCysAlaGln 177
DB 423 GTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 481
QY 178 AlaSerCysAlaThrGlyAlaThrLeuThrLeu---CysLeuTyrAsnProHisGlyAsn 196
DB 482 GTGCTGTCAACACAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 541
QY 197 ValGlnGlyGlnSerProTyr 203
DB 542 TTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 562

```

RESULT 8

US-09-938-842A-2047

Sequence 2047, Application US/09938842A

Patent No. US20020160378A1

GENERAL INFORMATION:

APPLICANT: Harper, Jeff

APPLICANT: Kieps, Joel

APPLICANT: Wang, Xun

APPLICANT: Zhu, Tong

TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING

TITLE OF INVENTION: SAME, AND METHODS OF USE

FILE REFERENCE: SCRI1300-3

CURRENT APPLICATION NUMBER: US/09/938,842A

PRIOR FILING DATE: 2001-08-24

PRIOR APPLICATION NUMBER: US 60/227,866

PRIOR FILING DATE: 2000-08-24

PRIOR APPLICATION NUMBER: US 60/264,647

PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 2047
LENGTH: 486
TYPE: DNA
ORGANISM: Arabidopsis thaliana
US-09-938-842A-2047

Alignment Scores:
Pred. No.: 1.5e-17 Length: 486
Score: 288.00 Matches: 64
Percent Similarity: 51.23% Conservative: 19
Best Local Similarity: 39.51% Mismatches: 65
Query Match: 26.54% Indels: 14
DB: 9 Gaps: 5

US-09-832-320-2 (1-203) x US-09-938-842A-2047 (1-486)

```

QY 42 ValLeuMetProGlyGlyAlaGlyAlaValThrLysAlaGlnGlnGlyThreGlySer 61
DB 40 GTAGCTCTTGTAGGCTGCTGTCTTCCCTCGAAGCTCAAGAT----- 84
QY 62 GlySerAsnAlaThrAlaAspGluTyrLeuAlaProHisAsnGlnAlaArgAlaAlaVal 81
DB 85 -----ACCCACAAGATTACTAAGGTTCCACACACAGCGCAGCGAGCGGTA 132
QY 82 GlyValAlaProLeuAlaGlyTyrPheAlaGlyLeuAlaSerAlaAlaAlaGlyThyValAla 101
DB 133 GCGGTAGGTCCTCAGTACAGTGGGAGAGAGGTTGCA---GCTTATCTCTCGAGTACCCA 189
QY 102 GlnGlnAlaArgAlaGlnGlyGlyCysAlaPheAlaAspValGlyAlaSerProTyrGlyAla 121
DB 190 GACAACTAAGAA---GGCACTGCAAGCTCATGACTGTG---GCGCTTACGGGAA 243
QY 122 AsnGlnGlyTyrPheAlaSerTyrArgAlaAlaArgProAlaGlnValAlaLeuTyrValAla 141
DB 244 AACTTACGCGGGGTAGCGGTACTGTCTGCGCTCCGCGCGCGCGCGCGCGCGCGCGCGCG 303
QY 142 GluGlyArgTyrTyrHisAlaAsnThrCysAlaAlaGlyArgGlnCysGlyThr 161
DB 304 GAGAGGCTAATCACTACACTACGCTGCGCAACACTGC-----AAGGAGTTTGTGTAC 357
QY 162 TyrThrGlnValAlaThrPheAsnThrAlaGlnValGlyCysAlaGlnAlaSerCysAla 181
DB 358 TACACTCAAGTGTGTTGAGAAAGTCACTGAGACTGCGATGTCGCAAGTGAAGGTGTAAC 417
QY 182 ThrGlyAlaThrLeuThrLeuThrLeuThrLeuThrLeuThrLeuThrLeuThrLeuThr 201
DB 418 AATGGTGAACCAATACATGATGCACTATGATCGTGGGAATATGTGAAACGAGAG 477
QY 202 ProTyr 203
DB 478 CCATAC 483

```

RESULT 9

US-09-887-576-608

Sequence 608, Application US/09887576

Patent No. US20020144047A1

GENERAL INFORMATION:

APPLICANT: Budworth, P.

APPLICANT: Brown, D.

APPLICANT: Chang, H.

APPLICANT: Zhu, T.

APPLICANT: Han, B.

APPLICANT: Wang, X.

TITLE OF INVENTION: Promoters for regulation of plant expression

FILE REFERENCE: 1360.001US1

CURRENT APPLICATION NUMBER: US/09/887,576

PRIOR FILING DATE: 2001-06-25

PRIOR APPLICATION NUMBER: US 60/213,848

```
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/214,087
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/258,692
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 875
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 608
; LENGTH: 738
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(738)
; OTHER INFORMATION: n = A,T,C or G
US-09-887-576-608

Alignment Scores:
Pred. No.: 2,486-17 Length: 738
Score: 288.00 Matches: 64
Percent Similarity: 51.23% Conservative: 19
Best Local Similarity: 39.51% Mismatches: 65
Query Match: 26.54% Indels: 14
DB: 10 Gaps: 5

US-09-832-320-2 (1-203) x US-09-887-576-608 (1-738)
OY 42 ValLeuMeTProGlyGlyAlaGlyAlaValThrLysAlaGlnGlnGlyThrGlySer 61
DB 52 GTAGGCTCTGTAGTGTCTTGTCTTCCCTCGAAGCTCAAGAT----- 96
OY 62 GlySerAsnAlaThrAlaAspGluTyrLeuAlaProHisAsnGlnAlaArgAlaAlaVal 81
DB 97 -----AGCCACAGATTAATCTAAGGTTCAACACGAGCGAGGCGGTA 144
OY 82 GlyValAlaProLeuArgTyrPaspAsnAlaGlyLeuAlaSerAlaAlaAlaGlyThrValAla 101
DB 145 GGGGTAGTCCATGCGAGTGGAGCGAGGAGGTTGCA---GCCATGCTCGGAGCTACGCCA 201
OY 102 GlnGlnArgTyrGlnGlyCysAlaPheAlaAspValGlyAlaSerProTyrGlyAla 121
DB 202 GAACACTACAGA---GGCAACTGACAGCTCATACACTCTGT---GGGCTTACGGGGAA 255
OY 122 AsnGlnGlyTrpAlaSerTyrArgAlaArgProAlaGluValAlaLeuThrValAla 141
DB 256 AACTTAGCCTGGGTAGCGGTGACTTGTCTGCCGCTCCGCCGTAACATGTGGTTAGC 315
OY 142 GlnGlyArgTyrTyrThrHisAlaAsnAsnThrCysAlaAlaGlyArgGlnCysGlyThr 161
DB 316 GAGAAAGGCTAATCAACAATGCTGCGACAGCTG-----AATGAGTTTGTGGTCAAC 369
OY 162 TyrThrGlnValValTrrPArgAsnThrAlaGluValGlyCysAlaGlnAlaSerCysAla 181
DB 370 TACACTCAAGTTGTGGTGAAGAGTCAGTGAAGCTGGAGTGGCAAGTGAGTGAAC 429
OY 182 ThrGlyAlaThrLeuThrLeuCysLeuTyrAsnProHisGlyAsnValGlnGlyGlnSer 201
DB 430 AATGGTGAACCATATATGATGTCACATGATTCCTCGTGGGAATTAAGTGAACGAGAAG 489
OY 202 ProTyr 203
DB 490 CCATAC 495

RESULT 10
US-09-887-576-618
; Sequence 618, Application US/09887576
; Patent No. US20020144047A1
; GENERAL INFORMATION:
; APPLICANT: Budworth, P.
; APPLICANT: Brown, D.
; APPLICANT: Chang, H.
; APPLICANT: Zhu, T.
; APPLICANT: Han, B.
```

```
; APPLICANT: Wang, X.
; APPLICANT: Cooper, Bret
; TITLE OF INVENTION: Promoters for regulation of plant expression
; FILE REFERENCE: 1360.001US1
; CURRENT APPLICATION NUMBER: US/09/887,576
; CURRENT FILING DATE: 2001-06-25
; PRIOR APPLICATION NUMBER: US 60/213,848
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/214,087
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/258,692
; PRIOR FILING DATE: 2000-12-29
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 618
; LENGTH: 757
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-887-576-618

Alignment Scores:
Pred. No.: 2,566-17 Length: 757
Score: 288.00 Matches: 64
Percent Similarity: 51.23% Conservative: 19
Best Local Similarity: 39.51% Mismatches: 65
Query Match: 26.54% Indels: 14
DB: 10 Gaps: 5

US-09-832-320-2 (1-203) x US-09-887-576-618 (1-757)
OY 42 ValLeuMeTProGlyGlyAlaGlyAlaValThrLysAlaGlnGlnGlyThrGlySer 61
DB 52 GTAGGCTCTGTAGTGTCTTGTCTTCCCTCGAAGCTCAAGAT----- 96
OY 62 GlySerAsnAlaThrAlaAspGluTyrLeuAlaProHisAsnGlnAlaArgAlaAlaVal 81
DB 97 -----AGCCACAGATTAATCTAAGGTTCAACACGAGCGAGGCGGTA 144
OY 82 GlyValAlaProLeuArgTyrPaspAsnAlaGlyLeuAlaSerAlaAlaAlaGlyThrValAla 101
DB 145 GGGGTAGTCCATGCGAGTGGAGCGAGGAGGTTGCA---GGCTATGCTCGGAGCTACGCCA 201
OY 102 GlnGlnArgTyrGlnGlyCysAlaPheAlaAspValGlyAlaSerProTyrGlyAla 121
DB 202 GAACACTACAGA---GGCAACTGACAGCTCATACACTCTGT---GGGCTTACGGGGAA 255
OY 122 AsnGlnGlyTrpAlaSerTyrArgAlaArgProAlaGluValAlaLeuThrValAla 141
DB 256 AACTTAGCCTGGGTAGCGGTGACTTGTCTGCCGCTCCGCCGTAACATGTGGTTAGC 315
OY 142 GlnGlyArgTyrTyrThrHisAlaAsnAsnThrCysAlaAlaGlyArgGlnCysGlyThr 161
DB 316 GAGAAAGGCTAATCAACAATGCTGCGACAGCTG-----AATGAGTTTGTGGTCAAC 369
OY 162 TyrThrGlnValValTrrPArgAsnThrAlaGluValGlyCysAlaGlnAlaSerCysAla 181
DB 370 TACACTCAAGTTGTGGTGAAGAGTCAGTGAAGCTGGAGTGGCAAGTGAGTGAAC 429
OY 182 ThrGlyAlaThrLeuThrLeuCysLeuTyrAsnProHisGlyAsnValGlnGlyGlnSer 201
DB 430 AATGGTGAACCATATATGATGTCACATGATTCCTCGTGGGAATTAAGTGAACGAGAAG 489
OY 202 ProTyr 203
DB 490 CCATAC 495

RESULT 11
US-10-078-929-85
; Sequence 85, Application US/10078929
; Patent No. US20020152497A1
; GENERAL INFORMATION:
; APPLICANT: Rafalski, Antoni
; APPLICANT: Miao, Guo-Hua
```



```

: APPLICANT: Falco, Saverio Carl
: APPLICANT: Sakai, Hajime
: APPLICANT: Famodu, Omolayo O.
: APPLICANT: Odell, Joan T.
: APPLICANT: Meyers, Blake
: APPLICANT: Thorpe, Catherine
: APPLICANT: Weng, Zude
: TITLE OF INVENTION: Nucleic Acid Fragments Encoding Proteins Involved in
: FILE REFERENCE: HB137 US NA
: CURRENT FILING DATE: 2002-02-19
: PRIOR APPLICATION NUMBER: 09/566,394
: PRIOR FILING DATE: 2000-05-05
: PRIOR APPLICATION NUMBER: 60/133038
: PRIOR FILING DATE: 1999-05-07
: PRIOR APPLICATION NUMBER: 60/133042
: PRIOR FILING DATE: 1999-05-07
: PRIOR APPLICATION NUMBER: 60/133427
: PRIOR FILING DATE: 1999-05-11
: PRIOR APPLICATION NUMBER: 60/133437
: PRIOR FILING DATE: 1999-05-11
: PRIOR APPLICATION NUMBER: 60/133428
: PRIOR FILING DATE: 1999-05-11
: PRIOR APPLICATION NUMBER: 60/133438
: PRIOR FILING DATE: 1999-05-11
: PRIOR APPLICATION NUMBER: 60/133436
: PRIOR FILING DATE: 1999-05-11
: PRIOR APPLICATION NUMBER: 60/137667
: PRIOR FILING DATE: 1999-06-04
: NUMBER OF SEQ ID NOS: 208
: SOFTWARE: Microsoft Office 97
: SEQ ID NO 85
: LENGTH: 714
: TYPE: DNA
: ORGANISM: Oryza sativa
US-10-078-929-85

Alignment Scores:
Pred. No.: 2,92e-17 Length: 714
Score: 287.00 Matches: 70
Percent Similarity: 52.57% Conservative: 22
Best Local Similarity: 40.00% Mismatches: 71
Query Match: 26.45% Indels: 12
DB: 12 Gaps: 7

US-09-832-320-2 (1-203) x US-10-078-929-85 (1-714)
QY 33 AlaProAlaProThrHisGlyAlaArgValLeuMetProGlyGlyAlaGlyAlaValThr 52
Db 22 GCACCTTCACAAAGTCAGCCGCGCGCGCTC-----GCCGTGGCATCTCG 69
QY 53 LysAlaGlnGlnGlyGlyThrGlySerGlySerAsnAlaThrAlaAspGluTyrLeuAla 72
Db 70 CTGGCCATGGCGGCCACACCCACCTCGGCGCGCAAGACCGCGCATAGCTAAC 129
QY 73 ProHisGlnGlnAlaArgAlaValGlyValAlaProLeuArgTyrPasnAlaGlyLeu 92
Db 130 CTGCACAAACAGCGCGCGCGCGCGCTCGCGCGGAGCTGGAGCCCAAGCTC 189
QY 93 AlaSerAlaAlaGlyThrValAlaGlnGlnArgTyrGlnGlyCysAlaPheAla 112
Db 190 GCCAGCTTCGCGAGACGCTACGCGCC-----AAGCGCGCGCGACTGCCGCTCAG 243
QY 113 AspValGlyAlaSerProTyrGlyAlaAsnGlnGlyTyrPalaSerTyr--ArgAla--- 130
Db 244 CACTCCCGGCG--GGCGCGTACGCGCGAACAATCTTGGGGCTCGCGCGCGCGCGCTGG 300
QY 131 ArgProAlaValValAlaLeuTyrValAlaGlnGlyArgTyrTyrThrHisAlaAsn 150
Db 301 AGCGCGCGACGCGGCGGTGCTGCGTGGCGGCGAGAAAGAACTACCATACGACAC 360
QY 151 AsnThrCysAlaAlaGlyArgGlnCysGlyTyrThrGlnValValTTPArgAsnThr 170
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Db 361 AACACGTGCACCCCGGCAAGGTGTGCGGCACACACACCGAGCGGTGCGCAAGCTCG 420
QY 171 AlagIuValGlyCysAlaGlnAlaSerCysAlaThr-----GlyAlaThrLeuThrIleu 188
Db 421 GTGGCGATCGGGTGGCGCGCGCGCTGCTGCGCGCGGCAACCGCGCGCTTCATCACC---- 477
QY 189 CysLeuTyrAsnProHisGlnGlnValGlnGlyGlnSerProTyr 203
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RESULT 12
US-10-078-929-99
: Sequence 99, Application US/10078929
: Patent No. US20020152497A1
: GENERAL INFORMATION:
: APPLICANT: Rafalski, Antoni
: APPLICANT: Miao, Guo-Hua
: APPLICANT: Falco, Saverio Carl
: APPLICANT: Sakai, Hajime
: APPLICANT: Famodu, Omolayo O.
: APPLICANT: Odell, Joan T.
: APPLICANT: Meyers, Blake
: APPLICANT: Thorpe, Catherine
: APPLICANT: Weng, Zude
: TITLE OF INVENTION: Nucleic Acid Fragments Encoding Proteins Involved in
: FILE REFERENCE: HB137 US NA
: CURRENT FILING DATE: 2002-02-19
: PRIOR APPLICATION NUMBER: 09/566,394
: PRIOR FILING DATE: 2000-05-05
: PRIOR APPLICATION NUMBER: 60/133038
: PRIOR FILING DATE: 1999-05-07
: PRIOR APPLICATION NUMBER: 60/133042
: PRIOR FILING DATE: 1999-05-07
: PRIOR APPLICATION NUMBER: 60/133427
: PRIOR FILING DATE: 1999-05-11
: PRIOR APPLICATION NUMBER: 60/133437
: PRIOR FILING DATE: 1999-05-11
: PRIOR APPLICATION NUMBER: 60/133428
: PRIOR FILING DATE: 1999-05-11
: PRIOR APPLICATION NUMBER: 60/133438
: PRIOR FILING DATE: 1999-05-11
: PRIOR APPLICATION NUMBER: 60/133436
: PRIOR FILING DATE: 1999-05-11
: PRIOR APPLICATION NUMBER: 60/137667
: PRIOR FILING DATE: 1999-06-04
: NUMBER OF SEQ ID NOS: 208
: SOFTWARE: Microsoft Office 97
: SEQ ID NO 99
: LENGTH: 604
: TYPE: DNA
: ORGANISM: Triticum aestivum
US-10-078-929-99

Alignment Scores:
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Score: 280.50 Matches: 70
Percent Similarity: 48.98% Conservative: 26
Best Local Similarity: 35.71% Mismatches: 61
Query Match: 25.85% Indels: 39
DB: 12 Gaps: 8

US-09-832-320-2 (1-203) x US-10-078-929-99 (1-604)
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QY 35 AlaProThrHisGlyAlaArgValLeuMetProGlyGlyAlaGlyAlaValThrLysAla 54
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?      LENGTH: 783
?      TYPE: DNA
?      ORGANISM: Zea mays
?      FEATURE:
?       NAME/KEY: unsure
?       LOCATION: (760)
?    US-10-078-929-81

Alignment Scores:
Pred. No.:           3,49e-15          Length:         783
Score:              264.00             Matches:         69
Percent Similarity: 51.41%            Conservative:   22
Best Local Similarity: 38.98%        Mismatches:     76
Query Match:         24.33%           Indels:         10
DB:                  12               Gaps:           7

US-09-832-320-2 (1-203) x US-10-078-929-81 (1-783)
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QY      52 ThLYrAlagInchneIyGLyThngLyserGIySerAsnaIAthrAlaspoluryleu
Db      87 GGCGGGCAGTAGATGGCCGGCACCGCTCGCCGCAGAAC--ACGCCAGAGATTGCTG
QY      72 AlAPRHiASnglnAlArGAalAlAvalAGLyValAlAPRoLeuarTrTPsaNlaGLy
Db      144 ATCTGCACAMCCGGCGGGCGGGCGGAGCGAGCATTTCTGGGGCTGCTGGGAGCCAGG
QY      92 LeuAlAserrAlAlAalAGLyThrvAlAglachnImArgnsIngLySLySAlAbhe
Db      204 GTGGCCAGGTACCcGcGAGAActAcCGcGc-----AAgGcCcGggAGTcGcgGctG
QY      112 AlaSPVaIGLyAlasePrOtyrGLyAlaSnGInGLyTRPaLaSetyr--ArGLa
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QY      131 ---ARPrAlaGlIVaLVaLAldEutRPvAlAlaaGInLyArGrTyrrThrHIsia
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QY      150 AsnaSnThrCYsAlaAlaGLyArGGLncSGLyThrTYrrHgInVAlVRParGsn
Db      375 AGCAACACTGCGACCCCgcGCAAGGTgtGGCGCCACTracAGcAGSTGTGTGGCGAGG
QY      170 --ThrlaGlUvaLIgyCySaGlaGlnAlaseCYsSalatrngLy--AlatrhleuthrL
Db      435 TGTCACCCGCATCGGCTGGCGGGCGCGCTGCTGTCCGCCGAACCGCGGCGCTTCATCG
QY      188 eucSYeuTryAnPProHISglyasnVAInsglYInsErProTyR
Db      495 TCCTCAGACTACGACCccCGGCAACGTCAAGCGCCAGCCCGCTTC
RESULT 14
US-09-840-479-14
? Sequence 14, Application US/09840479
? Patent No. US20010025380A1
? GENERAL INFORMATION:
? APPLICANT: Crane, Virginia
? TITLE OF INVENTION: Family Of Maize PR-1 Genes And Promoters
? FILE REFERENCE: 5718-32, 035718/175219
? CURRENT APPLICATION NUMBER: US/09/440,479
? PRIOR FILING DATE: 2001-04-23
? PRIORITY APPLICATION NUMBER: 09/257,583
? PRIOR FILING DATE: 1999-02-25
? NUMBER OF SEQ ID NOS: 37
? SOFTWARE: patentin Ver. 2.0
? SEQ ID NO 14
? LENGTH: 806
? TYPE: DNA
? ORGANISM: Zea mays
? FEATURE:
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•
•
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GenCore version 5.1.4.p5.4578
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OM protein - nucleic search, using frame_plus_p2n model

Run on: February 22, 2003, 02:00:38 : Search time 228 Seconds
(without alignments)
2005.069 Million cell updates/sec

Title: US-09-832-320-2

Perfect score: 1085

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Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-NO_XLPHY -NO_MAMP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMECUT=120
-WARN_TIMECUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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- 2: /SIDS2/gcgdata/geneSeq/geneSeq-emb1/NA1981.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1085	100.0	612	ABA96418	Maize PRI-C10 ccd1
2	1085	100.0	898	ABA96417	Maize PRI-C10 enco
3	348.5	32.1	679	AA049084	Arabidopsis thalia
4	347.5	32.0	683	AA037078	Arabidopsis thalia
5	333	30.7	749	AA021207	Zea mays pathogene
6	331	30.5	731	AA099804	PR-1 like gene PR-
7	322	29.7	846	ABL59008	Nucleotide sequenc
8	304	28.0	679	ABL59001	PR-1b cDNA sequenc
9	304	28.0	771	AA006181	Tobacco PR-1b gene
10	304	28.0	771	AA062806	PR-1b protein enco
11	297.5	27.4	779	AA047173	Arabidopsis thalia
12	296	27.3	696	AA006182	PR-1c cDNA cloned
13	286	27.3	696	AA02807	Tobacco PR-1c gene
14	286	27.3	696	AA02807	PR-1c protein enco
15	286	27.3	696	AA02807	Nicotiana tabacum
16	295	27.2	721	AA091021	Zea mays pathogene
17	292.5	27.0	866	AA021191	Nucleotide sequenc
18	288	26.5	664	ABL59002	PR-1b cDNA cloned
19	288	26.5	860	AA099807	Tobacco PR-1b gene
20	288	26.5	860	AA062839	PR-1b protein enco
21	288	26.5	860	AA062839	Arabidopsis PR-1 g
22	287	26.5	1363	AA091026	Arabidopsis PR-1 p
23	286.5	26.4	447	AA040410	Genomic sequence o
24	286	26.4	780	AA045155	Potato infection 1
25	286	26.4	809	AA006180	Arabidopsis thalia
26	286	26.4	809	AA062805	Tobacco PR-1a gene
27	286	26.4	809	AA072997	PR-1a protein enco
28	286	26.4	2038	AA090367	Fragment of tobacco
29	286	26.4	2038	AA062887	Tobacco PR-1a gene
30	286	26.4	2038	AA072998	PR-1a protein enco
31	285	26.3	2038	AA030663	Tobacco PR-1a gene
32	282	26.0	772	AA091019	Fragment of tobacco
33	281.5	25.9	480	AA031653	Nicotiana tabacum
34	277.5	25.6	480	AA031652	Pathogenesis-relat
35	264	24.3	806	AA021194	Pathogenesis-relat
36	260	24.0	2090	AA090368	Zea mays pathogene
37	260	24.0	2256	AA062853	Fragment of tobacco
38	260	24.0	2256	AA072990	Tobacco PR-1' gene
39	259.5	23.9	483	AA031654	Tobacco PR-1' gene
40	257	23.7	493	AA046773	Pathogenesis-relat
41	256.5	23.6	480	AA031656	Arabidopsis thalia
42	248	22.9	1260	AA004693	Pathogenesis-relat
43	246	22.7	561	AA028346	Promoter of the in
44	244.5	22.5	453	AA031655	A. thaliana gene 1
45	232.5	21.4	940	AA052190	Pathogenesis-relat

ALIGNMENTS

RESULT 1

ABA96418 standard; CDNA; 612 BP.

ABA96418:

02-APR-2002 (first entry)

Maize PRI-C10 coding sequence SEQ ID NO 3.

Maize: pathogen-related; PRI-C10; plant; transgenic; gene; ss.

Zea mays.

Key Location/Qualifiers

FT 1..612 /tag= a

FT CDS /product= "PRI-C10"

XX US2001049834-A1.
 XX 06-DEC-2001.
 XX 10-APR-2001; 2001US-0832320.
 XX 10-APR-2000; 2000US-195801P.
 XX (CRAN/) CRANE E H.
 XX (CRAN/) CRANE V C.
 XX Crane EH, Crane VC;
 XX WPI; 2002-121407/16.
 XX P-PSDB; AAM48742.
 XX New nucleic acid encoding a pathogen-related protein isolated from
 PT maize and designated PRI-C10, useful for transforming plants for
 PT enhanced disease resistance.
 XX Claim 1; Page 32; 34pp; English.
 XX The invention relates to an isolated nucleic acid encoding a
 CC pathogen-related protein PRI-C10. The nucleic acid is used to transform
 CC plants for enhanced disease resistance.
 XX Sequence 612 BP; 80 A; 231 C; 239 G; 62 T; 0 other;
 SQ

Alignment Scores:
 Pred. No.: 3,41e-69 Length: 612
 Score: 1085.00 Matches: 203
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 24 Gaps: 0

US-09-832-320-2 (1-203) x ABA96418 (1-612)

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 DB 1 ATGGGGCACTGGCGGCGACGACACACCTCTCTCGCCGCGCCATGGCGACGGCG 60
 OY 21 CysLeuLeuLeuAlaThrLeuLeuAlaLeuCysAlaAlaProAlaProHisIleGlyAla 40
 DB 61 TGGTGGCTCTGGCCACCTCTGGCGCTGGCGCGCGCGCGCGACCGACGGCGCG 120
 OY 41 ArgValLeuMetProGlyIleGlyAlaValThrLysAlaGlnGlnGly1yThrGly 60
 DB 121 GCGGTCCTCATGGCGGGCGGGCGGGGTGACCAAGCGAGCGGTGGCGACCGGC 180
 OY 61 SerGlySerAsnAlaThrAlaAspGluTyrLeuAlaProHisAsnGlnAlaArgAlaAla 80
 DB 181 ACCGGCACCAACGGGACGGGAGAGTACTGGCGCGCGACCAAGCGGGCGGGCGG 240
 OY 81 ValGlyValAlaProLeuArgTyrPasnAlaGlyLeuAlaSerAlaAlaIleGlyThrVal 100
 DB 241 GGGGCGGTGGCGCGCGGTGGGAACGGCGGCTGGCGGGCGCGGGGACGGTG 300
 OY 101 AlaGlnGlnArgArgGlnGlnGlyCysAlaPheAlaAspValGlyLaseProTyrGly 120
 DB 301 GGGGACGAGGGGCGGAGGGGCGGTGGCGGTGGCGAGCTGGGGCGACGCCCTACGGC 360
 OY 121 AlaAsnGlnGlyTyrPalaSerTyrArgAlaArgProAlaGluValAlaAlaLeuTyrVal 140
 DB 361 GCGAACCAAGGGGTGGGAGCTACCGCGCGCGCGCGAGGTGGCGCTGGGGTG 420
 OY 141 AlaGluGlyArgGlyTyrThrHisAlaAsnThrCysAlaAlaGlyLysGlnGly 160
 DB 421 GGGGAGGGGGGTACTACACCGACCAACACAGCGGGCGCGGGGAGGAGTGGCGG 480
 OY 161 ThrTyrThrGlnValValTyrPargAsnThrAlaGluValGlyCysAlaGlnAlaLaseCys 180

DB 481 ACGTACACGACAGTGTGTGGCGCAACACCGCGAGGTGGGTGGCGGACGAGTGC 540
 OY 181 AlaThrGlyAlaThrLeuThrLeuCysLeuTyrAsnProHisGlyAsnValGlnGly 200
 DB 541 GCCAGGGGCGGCGGCTGCTGTGGTGTACACCGCGACGCGACGAGTGGAGGGCCAG 600
 OY 201 SerProTyr 203
 DB 601 AGCCCTTAC 609

RESULT 2
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 ID ABA96417 standard; cDNA; 898 BP.
 XX ABA96417;
 AC 02-APR-2002 (first entry)
 DT 02-APR-2002 (first entry)
 XX Maize PRI-C10 encoding cDNA SEQ ID NO 1.
 DE Maize; pathogen-related; PRI-C10; plant; transgenic; gene; ss.
 XX Zea mays.
 OS
 XX Key Location/Qualifiers
 FH 63..674
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XX US2001049834-A1.
 XX 06-DEC-2001.
 XX 10-APR-2001; 2001US-0832320.
 XX 10-APR-2000; 2000US-195801P.
 XX (CRAN/) CRANE E H.
 XX (CRAN/) CRANE V C.
 XX Crane EH, Crane VC;
 XX WPI; 2002-121407/16.
 XX P-PSDB; AAM48742.
 XX New nucleic acid encoding a pathogen-related protein isolated from
 PT maize and designated PRI-C10, useful for transforming plants for
 PT enhanced disease resistance.
 XX Claim 1; Page 30-31; 34pp; English.
 XX The invention relates to an isolated nucleic acid encoding a
 CC pathogen-related protein PRI-C10. The nucleic acid is used to transform
 CC plants for enhanced disease resistance.
 XX Sequence 898 BP; 161 A; 295 C; 309 G; 133 T; 0 other;
 SQ

Alignment Scores:
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 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 24 Gaps: 0

US-09-832-320-2 (1-203) x ABA96417 (1-898)

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 DB 63 ATGGGGCACTGGCGGCGACGACACCTCTCTCTGCTCCCGCGCATGGCGACGGCG 122
 OY 21 CysLeuLeuLeuAlaThrLeuLeuAlaLeuCysAlaAlaProAlaProHisIleGlyAla 40

Db	123	TGCTTCTCTCTTCGGCCACCCTCTCTCGCGCTCTGCGCCGCCGCCGCCGCCACCCACCGCGCGC	182
Qy	41	ATGValLeMePeProGlyGlyAlaGlyAlaValThrLysAlaGlnGlnGlyGly	60
Db	183	CGCGTCTCATCTCCGGGCGCGCGCGCGGTGACCAAGCGCACAGGCTGGCACCGGC	242
Qy	61	SeGcISeSaMaIaThrAlaAspGluTyrLeuAlaProHisAsnGlnAlaArgAla	80
Db	243	AGGGGAGGAGACGACGCGCGGACGAGTACTGGCGCGCCACACCGACGCGCGCGCGC	302
Qy	81	ValGlyValAlaProLeuArgTyrPaspAlaGlyLeuAlaSerAlaAlaGlyThrVal	100
Db	303	GTGGGCGTGGCCCCCTCGCGGTGGAGACGGCGGCGCTGGTTCGGCGCGCGGAGCGGTG	362
Qy	101	AlaGlnGlnArgArgGlnGlnGlyCysAlaPheAlaAspValGlyAlaSerProTyrGly	120
Db	363	GCGCACACACGCGCGCGCGCGCGCGGTGCGCGCTTGGCGGACGTGGGGCCAGCCCTACGGC	422
Qy	121	AlaAsnGlnGlyTyrPalaSerTyrArgAlaArgProAlaGlyValAlaLeuTyrVal	140
Db	423	GCGAACACAGGGGTGGCGCACAGCTACCGCGCGCGCGCGCGAGGTGGTGGCTGGGCTG	482
Qy	141	AlaGlnGlyArgTyrTyrThrHisAlaAsnAsnThrCysAlaAlaGlyArgGlnCysGly	160
Db	483	GCGGAGGGCGGGTACTATACACCCAGCCACACACAGCTGGCGCGCGGGCGGCACTGGCGC	542
Qy	161	ThrTyrThrGlnValValTyrPArgAsnThrAlaGluValGlyCysAlaGlnAlaSerCys	180
Db	543	ACGTATACACGACAGGTGTGGCGGACACACCGCGAGGTGGGTGGCGCGCACGCTGC	602
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AC	AAC49084;		
NC	18-OCT-2000	(first entry)	
XX	Arabidopsis thaliana DNA fragment SEQ ID NO: 59865.		
De	Hybridisation assay; genetic mapping; gene expression control;		
KW	Protein identification; signal transduction pathway;		
KM	metabolic pathway; promoter; termination sequence; ss.		
OS	Arabidopsis thaliana.		
XX	EP1033405-A2.		
PN	06-SEP-2000.		
PD	25-FEB-2000; 2000EP-0301439.		
XX	25-FEB-1999; 99US-0121825.		
PR	05-MAR-1999; 99US-0123180.		
PR	09-MAR-1999; 99US-0123548.		
PR	23-MAR-1999; 99US-0125768.		
PR	25-MAR-1999; 99US-0126264.		
PR	29-MAR-1999; 99US-0126785.		
PR	01-APR-1999; 99US-0127462.		
PR	06-APR-1999; 99US-0128234.		
PR	08-APR-1999; 99US-0128714.		
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PR	19-APR-1999; 99US-0130077.		
PR	21-APR-1999; 99US-0130449.		
PR	23-APR-1999; 99US-0130510.		

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PR 29-OCT-1999; 99US-0162142.
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Alignment Scores:

Pred. No.:	1,42e-16	Length:	679
Score:	348.50	Matches:	69
Percent Similarity:	60.14%	Conservative:	17
Best Local Similarity:	48.25%	Mismatches:	54
Query Match:	32.12%	Indels:	3
DB:	21	Gaps:	2

US-09-832-320-2 (1-203) x AAC49084 (1-679)

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OY 64 AenAlaThrAlaAspGluTyrLeuAlaProHisAsnGlnAlaArgAlaIaValGlyVal 83
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DB 201 TCTGCAGCAGCTTAAGCTTTTCACGATGCGACACAAAGCCAGCCATGCTGCTT 260
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OY 84 AlaProLeuArgTyrPAsnAlaGlyLeuAlaSerAlaAlaIaGlyThrValAlaGlnGln 103
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OY 104 ArgArgGlnGlyGlyCysAlaPheAlaAspValGlyAlaSerProTyrGlyAlaAsnGln 123
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OY 124 GlyTyrPAlaSer-----TyrAlaArgAlaArgProAlaGlyValAlaLeuTyrValAla 141
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DB 381 CTTGGCGTAAAGGCGTTAGTACCCGTGACACCCGCTCTTCTGCTGAGACTTGGGTGAAG 440
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OY 142 GlnGlyArgTyrTyrHisAlaAsnThrCysAlaAlaGlyArgGlnCysGlyThr 161
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OY 182 ThrGlyAlaThr---LeuThrLeuCysLeuTyrAsnProHisGlyAsnValGlnGln 200
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DB 561 AAAGAGTCAAGGTTGTACCATTTGTTTACATTCCTCGGAATATATGGCCCA 620
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OY 201 SerProTyr 203
    |||||
DB 621 AAGCCTTAC 629
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RESULT 4
AAC37078 standard; DNA; 683 BP.
ID AAC37078:
XX
AC AAC37078:
XX
XX 17-OCT-2000 (first entry)
DT
XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 16099.


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XX Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
OS Arabidopsis thaliana.
XX EP1033405-A2.
PN
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
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OY	84	AlaProLeuAlaTrpAsnAlaCylLeuAlaLaserAlaAlaIaCylThValAlaGlnGln	103
		:::	
DB	261	CCACACACTGATTTGGGACGCGACGTTGGAGCTCTGCGAGCTGGCTGTACCCAG	320
OY	104	ArgArgIaGlnGlyCylValAlaPheAlaAspValAlaSerProIlyGlyValaAsnGln	123
DB	321	AGGACACAAAGAAAGTGTAAGTCTGGCCGAGCTGTAAACCTTGGAATTAAGCGCGACACAG	380
OY	124	GlyTrpAlaSer-----TyrArgAlaArgProAlaGluValAlaAlaLeuTrpValAla	141
DB	381	CTTTGGGCTTAAGGCTTACTAGCCCTGACACCCGCTCTCTGCTGGAGACTGGGTGAAG	440

Oy		142	GlnGlyAlaArgTyrThrThrHisAlaAsnSerThrCysAlaIleAlaGlyArgLncGlyCysGlyThr	161
Dd		441	GAGAAACCTTTTCACATATTATTAAGTCACACACGTGTCTCGCAACACACACAGTCGGGTT	500
Oy		162	TyrThrGlnValValITPRAgrASnThraIacGluValGlyCysAlaGlnAlaSerCysAla	181
Dd		501	TATTAACAACACTGCTCGAGAAACCTATAAAGCTCGGGTGCTCATAGCCACAGTGTACG	560
Oy		182	ThrGlyAlaThr--LeuThrCysLeuTyrisAnProHisGlyAsnValGlnGlyGln	200
Dd		561	AAAGAGTCACAGGTGTTCACACATTGTTTTTACACATCCCTCGGAATATATATGGCCAA	620
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Dd		621	AAGCCTTAC 629	
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ID	AAZ21207		AAZ21207 standard; DNA; 749 BP.	
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XX	DE	22-NOV-1999	(first entry)	
XX	XX	Zea mays pathogenesis-related class I PR-1#83 gene.		
KM	XX	Zea mays; maize; pathogenesis-related class I; PR-1; promoter;		
KM	XX	regulation; expression; disease resistance; genetic manipulation;		
KW	XX	tobacco mosaic virus; cucumber mosaic virus; ringspot virus;		
KW	XX	necrosis virus; maize dwarf virus; viroid; bacterial; insect;		
KW	XX	nematode; fungal; ss.		
OS	XX	Zea mays.		
XX	FH	Key	Location/Qualifiers	
FT	FT	CDS	92..583	
FT	FT	/tag=	a	
FT	FT	/product=	"PR-1#83"	
PN	XX		/note="pathogenesis-related class I protein"	
XX	XX	WO9943819-A1.		
PD	XX	02-SEP-1999.		
XX	PF	11-FEB-1999;	99WO-US03011.	
XX	PR	26-FEB-1998;	98US-0076100.	
PR	PR	27-MAR-1998;	98US-0079648.	
XX	PA	(PION-) PIONEER HI-BRED INT INC.		
XX	FI	Crane VC:		
XX	DR	WP1: 1999-527621/44.		
XX	P-PSDB:	AAZ29944.		
PT		New promoter sequences from pathogenesis-related genes of maize	-	
XX		Example 3; page 72-73; 86pp; English.		
XX	XX	AAZ21186 to AAZ21190 represents the nucleotide sequences for promoters		
CC	XX	isolated from a family of maize (zea mays) genes encoding pathogenesis		
CC	XX	related (PR-1) proteins. The promoters are useful for expressing		
CC	XX	heterologous genes (including genes for disease resistance) in plants,		
CC	XX	especially dicots, or monocots i.e. maize. The promoters are useful for		
CC	XX	the genetic manipulation of plants to exhibit specific phenotypes,		
CC	XX	particularly enhanced resistance to pathogen-caused disease. Pathogens		
CC	XX	include viruses such as tobacco or cucumber mosaic virus, ringspot		
CC	XX	viruses, necrosis virus, and maize dwarf virus, and viroids, bacteria,		
CC	XX	insects, nematodes and fungi. The present sequence encodes a maize		
CC	XX	PR-1 protein given in the present invention.		

Sequence 749 BP: 160 A; 235 C; 206 G; 148 T; 0 other;

Alignment Scores:

Pred. No.:	2,02e-15	Length:	749
Score:	333.00	Matches:	81
Percent Similarity:	48.13%	Conservative:	22
Best Local Similarity:	37.85%	Mismatches:	67
Query Match:	30.69%	Indels:	44
DB:	20	Gaps:	8

US-09-832-320-2 (1-203) x AA221207 (1-749)

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QY 5 ArgSerHisHisLeuLeuLeuProAla-----
DB 26 CGATCAGACATTGACCTTGCTGCTCATTAATTACTAGTTCATCAGCAACAA 85
QY 16 ---Prometala-----ThralAcysleuLeuAlaThrlLeuAlaLeuCyAla 32
DB 86 CAACAGATGGACCGACGCTAGCGCTCTAGCTGCGCATGAGCAGCATGCTGTG 145
QY 33 AlAProAlaProThrlHisGlyAlaArgValLeuMetProGlyAlaGlyAlaValThr 52
DB 146 GCGCCGTGC-----
QY 53 LysAlaGlnGlnGlyThrlGlySerGlySerAlaAlaThrlAlaAspGlyLeuAla 72
DB 155 -----ACGGCCAGAACTCGCCGAGAC---TACGTGGAC 187
QY 73 ProHisAsnGlnAlaArgAlaAlaValGlyAlaProLeuArgTrpAsnAlaGlyLeu 92
DB 188 CCGCAGAACGCGCGCGCGCGCGCTGCGCGCGCTGCTGCTGCGCGAGACCGCTC 247
QY 93 AlAserAlaAlaAlaGlyThrlValAlaGlnGlnAlaArgGlnGlyGlyAlaPheAla 112
DB 248 GCGCGGTACGCGCAGACGTCAGCGCGCGAG-----CGCCAGGCGCAGTCGACAGCTGATC 301
QY 113 AspValGlyAlaSerProTrpGlyAlaAsnGlnGlyTrpAlaSerTrpAlaGlyAla----- 130
DB 302 CACTCCGGC---GGCCCTACGCGCAGACCTCTTCTGCGCGCGCGCGCGACTGG 358
QY 131 ArgProAlaGlyAlaValAlaAlaLeuTrpValAlaGlnGlyArgTrpTrpHisAlaAsn 150
DB 359 TCGGGGTCCGACGCGCTGGGCTCTGCTGCTCGGAAAGAGTACTAGACCAAGACAC 418
QY 151 AsnTrpCysAlaAlaGlyArgGlnGlyThrlTrpGlnValValTrpAlaAsnThr 170
DB 419 AACAGCTGCGCGAGGCGAGGTGTGCGGCACACGACGAGGTGTGCGCGCGACTCC 478
QY 171 AlaGlyValGlyCysAlaGlnAlaSerCysAlaThrGlyAla---ThrLeuThrCys 189
DB 479 ACCGGCATGGCTGTGCTGCGCGCTCTGCGACAAACAGCGCGCGCTTCATCATCTGC 538
QY 190 LeuTrpAsnProHisGlyAsnValGlnGlyAsnProTrp 203
DB 539 ACCTACAAACCGCGCGCGAGCTGCTGCGGAGAGCCCTTAC 580

RESULT 6
AA099804
ID AA099804 standard; cDNA; 731 BP.
XX
AC AA099804;
XX
DT 20-JUN-1996 (first entry)
XX
DE PR-1 like gene PR-1mz.
XX
KW SAR, tobacco; protein-synthesis independent gene; cyclohexamide;
KW systemic acquired resistance response; anti-pathogen; plant protection;
KW maize; PR-1; ss.
OS
XX Zea mays.
XX
FH Key Location/Qualifiers

```

FT CDS 40..531
/*tag= a

PN W09519443-A2.

PD 20-JUL-1995.

PF 03-JAN-1995; 95WO-IB00002.

PR 13-JAN-1994; 94US-0181271.

PA (CIBA) CIBA GEIGY AG.

PI Alexander DC, Ryals JA, Uknes SJ, Ward ER;

DR WPI; 1995-263872/34.

PT P-PSDB; AAR91595.

PS New DNA contg. plant systemic acquired resistance genes - and
transgenic plants contg. them, impart disease and pest resistance,
also Arabidopsis gene promoter to control DNA transcription

Claim 21; Page 70; 85pp; English.

This sequence represents the DNA sequence of a maize PR-1 like gene.
CC PR-1mz. This sequence was isolated by screening a BTH-induced cDNA
CC library of maize. The library was screened using a probe matching to
CC the PR-1 barley clone HVPRI1B. This sequence, AA099800-099803 and
CC AA099805 are all used in recombinant/chimeric DNA molecules of the
CC invention. These sequences were isolated by differential screening of a
CC cDNA library, followed by analysis by Northern hybridisation to RNA in
CC the presence and absence of cyclohexamide. The genes are used in the
CC creation of transgenic plants. All of these sequences confer
CC anti-pathogenic properties to transgenic plants. Transgenic expression
CC of 2 or more of the recombinant molecules of the invention that encode
CC anti-pathogenic proteins provides a synergistic increase in plant
CC protection, and may also offer protection against a wider range of
CC pathogens.

Sequence 731 BP: 186 A; 212 C; 199 G; 134 T; 0 other;

Alignment Scores:

Pred. No.:	2.74e-15	Length:	731
Score:	331.00	Matches:	73
Percent Similarity:	50.27%	Conservative:	21
Best Local Similarity:	39.04%	Mismatches:	32
Query Match:	30.51%	Indels:	6
DB:	16	Gaps:	6

US-09-832-320-2 (1-203) x AA099804 (1-731)

```

QY 20 AlAcysleuLeuLeuAlaThrlLeuAlaLeuCyAlaAlaProAlaProThrlHisGly 39
DB 55 GCGTCTCTCTAGCTGTGCGCATGCGCATCTCTGCGCGCGCTGC----- 102
QY 40 AlaArgValLeuMetProGlyGlyAlaGlyAlaValThrLysAlaGlnGlnGlyThr 59
DB 102 -----
QY 60 GlySerGlySerAlaAlaThrlAlaAspGlyTrpLeuAlaProHisAsnGlnAlaArgAla 79
DB 103 ---ACGGCCAGAACTCGCCGAGAC---TACGTGAGACCGCAGACAGCGCGCGCGCC 156
QY 80 AlaValGlyValAlaProLeuArgTrpAsnAlaGlyLeuAlaSerAlaAlaAlaGlyThr 99
DB 157 GACGTGGGCGTGGCGCGGTCTCTGAGACACACCGTGGCGGTGACGCGCAGACTAC 216
QY 100 ValAlaGlnGlnArgArgGlnGlyGlyCysAlaPheAlaAspValGlyAlaSerProTrp 119
DB 217 GCGGCGCAG-----CGCCAGGCGACGCAAGCTGATCCACTCCGCGC---GGGCGCTAC 267
QY 120 GlyAlaAsnGlnGlyTrpAlaSerTrpAlaGlyAla-----ArgProAlaGlyValAlaAla 137

```

Db 268 GCGGAAACCTCTTCTGGGCTCCGCGCGACTGTGTGGCGTCCGAGCCGTGGG 327
 QY 138 LeuTPVAlAlaIGluGlyArgTyrThrHisAlaAsnProCysAlaIleArgTyr 157
 Db 328 TCCTGGGTGTCTGAGAACAGTACTACACACACACACACACACAGGAGGGGAG 387
 QY 158 GlncysglYthrTyrThrGlnValValTTParGAsnThrAlaGluValGlyCysAlaGln 177
 Db 388 GTGTGCGCGCACTACACGACGAGTGTGTGGCGCATCCGCCATCGCGTGGCCG 447
 QY 178 AlaSerCysAlaThrGlyAla---ThrLeuThrLeuCysLeuTyrAsnProHisGlyAsn 196
 Db 448 GTGCTGTGCGACACACACGCGCGCTTTCATCTGCACTACACACCGCGGAGAC 507
 QY 197 ValGlnGlyGlnSerProTyr 203
 Db 508 GTGCTGCGCGAGAGCCCTTAC 528
 RESULT 7
 ID ABL59008 standard; DNA; 846 BP.
 XX
 AC ABL59008;
 XX
 DT 20-AUG-2002 (first entry)
 XX
 DE Nucleotide sequence of an antibacterial protein.
 XX
 KW Antibacterial protein; microbe resistance; plant; gene; ss.
 XX
 OS Elaeis guineensis.
 XX
 FH Key Location/Qualifiers
 FT CDS 35..523
 FT /*tag= a
 FT /product= "antibacterial protein"
 FT
 PN JP2002095477-A.
 XX
 PD 02-APR-2002.
 XX
 PF 20-SEP-2000; 2000JP-0285905.
 XX
 PR 20-SEP-2000; 2000JP-0285905.
 XX
 PA (MITU) MITSUBISHI CHEM CORP.
 PA (BADA-) BADAN PENGKAJIAN DAN PENERAPAN TEKNOLOGI.
 PA (PAKR-) PT PAKRIE BROS.
 PA (BIOI-) BIOINDUSTRI KYOKAI SH.
 PA (DOKU-) DOKURITSU GYOSSEI HOJIN SANGYO GIJUTSU SO.
 XX
 DR WPI: 2002-439987/47.
 DR P-PSDB: ABB77767.
 XX
 PT New protein and its gene, useful for creating plants with high
 XX resistance to pathogenic microbes -
 XX
 PS Claim 3; Page 8-9; 13pp; Japanese.
 CC The present sequence encodes a polypeptide which has antibacterial
 CC activity. The antibacterial protein and its polynucleotide can be used
 CC for the creation of a plant with resistance against pathogenic microbes.
 XX
 SQ Sequence 846 BP; 218 A; 208 C; 214 G; 206 T; 0 other;
 Alignment Scores:
 Pred. No.: 1.4e-14 Length: 846
 Score: 322.00 Matches: 62
 Percent Similarity: 61.76% Conservative: 22
 Best Local Similarity: 45.59% Mismatches: 48
 Query Match: 29.68% Indels: 4
 DB: 24 Gaps: 3

US-09-832-320-2 (1-203) x ABL59008 (1-846)
 QY 69 GluTyrLeuAlaIleProHisAsnGlnAlaArgAlaValGlyValAlaProLeuArgTyr 88
 Db 122 GACTTGTGGAGCCGCGCCACACGACCCGCGCGCTCGCGCGCGCGCGGTGTGG 181
 QY 89 AsnAlaGlyLeuAlaSerAlaAlaAlaGlyThrValAlaGlnGlnArgArgGlnGly 108
 Db 182 GACAACACCGTGGGAGCGCTACGCCACGACCTACGCCAACCG-----CGAATCGGCGAC 235
 QY 109 CysAlaPheAlaIleArgValGlyAlaSerProTyrGlyAlaAsnGlnGlyThrAlaSerTyr 128
 Db 236 TGCAGCTGTGCTCAGCTCCGGC---GGACCGTACGCTAGAACCTCTTGTGGGATAGGT 292
 QY 129 ArgAla---ArgProAlaGluValAlaIleLeuTyrValAlaGluGlyArgTyrTyrThr 147
 Db 293 AGGAGTACACCGACGCGAGATGCTGTGAACCTTGTGGGTGATGAACAGCGTGTACGAC 352
 QY 148 HisAlaAsnAsnThrCysAlaAlaGlyArgGlnCysglYthrTyrThrGlnValValTTP 167
 Db 353 TACACGACCAACACTTGTGGCGCGGAGAGTGTGCGGTACTACACACCGAGTGTGTGG 412
 QY 168 ArgAsnThrAlaGluValGlyCysAlaGlnAlaSerCysAlaThrGlyAlaThrLeuThr 187
 Db 413 CGAGACTCCACCCACATCGGTGCGCTCGGGGTGAATGCAACAGTGGCGCATCTTATT 472
 QY 188 LeuCysLeuTyrAsnProHisGlyAsnValGlnGlyClnSerProTyr 203
 Db 473 ATCTGCACTACAAACCTTCGCGCAATATCTGTGGGACGAGCCCATAT 520
 RESULT 8
 ID ABL59001 standard; DNA; 679 BP.
 XX
 AC ABL59001;
 XX
 DT 20-AUG-2002 (first entry)
 XX
 DE Nucleotide sequence of an antibacterial protein.
 XX
 KW Antibacterial protein; antibacterial agent; food; plant; gene; ss.
 XX
 OS Wasabia japonica.
 XX
 FH Key Location/Qualifiers
 FT CDS 44..529
 FT /*tag= a
 FT /product= "antibacterial protein"
 FT
 PN JP2002095475-A.
 XX
 PD 02-APR-2002.
 XX
 PF 19-SEP-2000; 2000JP-0284178.
 XX
 PR 19-SEP-2000; 2000JP-0284178.
 XX
 PA (IWAT-) IWATE KEN.
 XX
 DR WPI: 2002-439986/47.
 DR P-PSDB: ABB77765.
 XX
 PT New antibacterial protein gene of Wasabia japonica -
 XX
 PS Claim 3; Page 12-13; 17pp; Japanese.
 CC The present sequence encodes an antibacterial protein of Wasabia
 CC japonica. The protein can be used in an antibacterial agent and a
 CC functional food.
 XX
 SQ Sequence 679 BP; 211 A; 142 C; 156 G; 170 T; 0 other;
 Alignment Scores:
 Pred. No.: 1.4e-14 Length: 679
 Score: 322.00 Matches: 62
 Percent Similarity: 61.76% Conservative: 22
 Best Local Similarity: 45.59% Mismatches: 48
 Query Match: 29.68% Indels: 4
 DB: 24 Gaps: 3

PT DNA encoding pathogenesis-related glucanase proteins - useful for
PT producing transgenic plants with enhanced disease or pest resistance
XX
PS Example 44: Column 175-176; 169pp; English.

XX The present invention describes a DNA molecule encoding a
CC pathogenesis-related (PR) protein having beta-1,3-glucanase activity
CC selected from PR-2, PR-2', PR-2'', PR-N, PR-O and PR-O'. Also described
CC are: (i) a chimeric gene comprising the above DNA molecule linked to a
CC heterologous promoter; (ii) a vector containing the chimeric gene;
CC (iii) a host cell containing the chimeric gene; (iv) a transgenic plant
CC containing the chimeric gene; and (v) a seed from the transgenic plant.
CC The DNA molecule is used to produce transgenic plants with enhanced
CC disease or pest resistance. The present sequence represents a tobacco
CC PR-1b protein encoding cDNA sequence from the present invention.

XX SQ Sequence 771 BP; 227 A; 148 C; 156 G; 240 T; 0 other;

Alignment Scores:

Score:	2,45e-13	Length:	771
Percent Similarity:	304.00	Matches:	64
Best Local Similarity:	56.55%	Conservative:	18
Query Match:	44.14%	Mismatches:	57
	28.02%	Indels:	6
DB:	20	Gaps:	3

US-09-832-320-2 (1-203) x AAV72998 (1-771)

QY 61 SerGlySerAsnAlaThrAlaAspGluTyrLeuAlaProHisnGlnAlaArgAlaAla 80
DB 111 TCTCATGCCCAAACTCTCAACACAGACTTGTGGATGCCCATACACAGCTCGTCAGAT 170
QY 81 ValGlyValAlaProLeuArgTyrPasnAlaGlyLeuAlaSerAlaAlaAlaGlyThrVal 100
DB 171 GTAGGCGTGAACCACTTAACCTGGGACACAGGAGAGACCATGACAAATTTATGTT 230
QY 101 AlAGlnGlnArgArgGlnGlyGlyCysAlaPheAlaAspAlaGlyAlaSerProTyrGly 120
DB 231 TCTCATGTGGCTGCAGACTGCACCTCGTACATTCAT-----GGCCAAATGCGC 281
QY 121 AlaAsn-----GlnGlyTyrPalaSerTyrArgAlaArgProAlaGluValAlaAlaLeu 138
DB 282 GAAGAACCTGACGAGGAGTGGCGATTATGACG---GCTGCTAGGCGCTCGAGATG 338
QY 139 TyrValAlaGlnGlyArgTyrTyrThrHisAlaAsnThrCysAlaAlaGlyArgGln 158
DB 339 TGGGTGATGAGAAACAGTACTATGACATGACTGAATCTGTGTCACAAAGACAGGTG 398
QY 159 CysGlyThrTyrThrGlnValValTyrPargAsnThrAlaGluValGlyCysAlaGlnAla 178
DB 399 TGTGACACTATACAGTACGCTGCTGCGTAACTCGGTGCTGTGATGCTCTAGCGTT 458
QY 179 SerCysAlaThrGlyAlaThrLeuThrLeuGlyCysLeuTyrAsnProHisGlyAsnValGln 198
DB 459 AAGTGGACAAATGGAGATATGTTCTCTCTTGCACATGATGCTCCAGGTAATGTCATA 518
QY 199 GlyGlnSerProTyr 203
DB 519 GCCCAAGTCCATAC 533

RESULT 12

ID AAC47173 standard: DNA; 779 BP.

XX AAC47173;

XX 18-OCT-2000 (first entry)

XX Arabidopsis thaliana DNA fragment SEQ ID NO: 52827.

XX Hybridisation assay; genetic mapping; gene expression control;

KM Protein identification; signal transduction pathway;

KW metabolic pathway; promoter; termination sequence; ss.

XX Arabidopsis thaliana.

XX EP1033405-A2.

XX 06-SEP-2000.

XX 25-FEB-2000; 2000EP-0301439.

XX 25-FEB-1999; 99US-0121825.

XX 09-MAR-1999; 99US-0123160.

XX 23-MAR-1999; 99US-0133548.

XX 23-MAR-1999; 99US-0125788.

XX 29-MAR-1999; 99US-0126264.

XX 01-APR-1999; 99US-0126785.

XX 06-APR-1999; 99US-0127462.

XX 08-APR-1999; 99US-0128234.

XX 16-APR-1999; 99US-0128714.

XX 19-APR-1999; 99US-0129845.

XX 21-APR-1999; 99US-0130077.

XX 23-APR-1999; 99US-0130449.

XX 23-APR-1999; 99US-0130510.

XX 28-APR-1999; 99US-0130891.

XX 30-APR-1999; 99US-0131449.

XX 30-APR-1999; 99US-0132048.

XX 04-MAY-1999; 99US-0132407.

XX 05-MAY-1999; 99US-0132484.

XX 05-MAY-1999; 99US-0132485.

XX 06-MAY-1999; 99US-0132486.

XX 06-MAY-1999; 99US-0132487.

XX 07-MAY-1999; 99US-0132863.

XX 11-MAY-1999; 99US-0134256.

XX 14-MAY-1999; 99US-0134218.

XX 14-MAY-1999; 99US-0134219.

XX 14-MAY-1999; 99US-0134321.

XX 14-MAY-1999; 99US-0134370.

XX 18-MAY-1999; 99US-0134768.

XX 19-MAY-1999; 99US-0134941.

XX 20-MAY-1999; 99US-0135124.

XX 21-MAY-1999; 99US-0135353.

XX 25-MAY-1999; 99US-0135629.

XX 27-MAY-1999; 99US-0136021.

XX 28-MAY-1999; 99US-0136392.

XX 01-JUN-1999; 99US-0136782.

XX 03-JUN-1999; 99US-0137222.

XX 04-JUN-1999; 99US-0137528.

XX 07-JUN-1999; 99US-0137724.

XX 08-JUN-1999; 99US-0138094.

XX 10-JUN-1999; 99US-0138540.

XX 14-JUN-1999; 99US-0138847.

XX 16-JUN-1999; 99US-0139119.

XX 16-JUN-1999; 99US-0139452.

XX 17-JUN-1999; 99US-0139453.

XX 17-JUN-1999; 99US-0139492.

XX 18-JUN-1999; 99US-0139454.

XX 18-JUN-1999; 99US-0139455.

XX 18-JUN-1999; 99US-0139456.

XX 18-JUN-1999; 99US-0139457.

XX 18-JUN-1999; 99US-0139458.

XX 18-JUN-1999; 99US-0139459.

XX 18-JUN-1999; 99US-0139460.

XX 18-JUN-1999; 99US-0139461.

XX 18-JUN-1999; 99US-0139462.

XX 18-JUN-1999; 99US-0139463.

XX 18-JUN-1999; 99US-0139750.

XX 18-JUN-1999; 99US-0139763.

XX 21-JUN-1999; 99US-0139817.

XX 22-JUN-1999; 99US-0139899.

XX 23-JUN-1999; 99US-0140353.

XX 23-JUN-1999; 99US-0140354.

XX 24-JUN-1999; 99US-0140695.

XX 28-JUN-1999; 99US-0140823.


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OY 169 AsnThrAlaGluValGlyCysAlaGlnAlaSerCysAlaThrGlyAlaThrLeu 188
DB 446 AACCTGGAGAGGTGGATGTGCAGAAAGTAGATGCACAACTGTTATTCACCT 505
OY 189 CysLeuTyrAsnProHisGlyAsnValGlnGlyGlnSerProTyr 203
DB 506 TGCACACTACGACTCTCCGCGTACTGGGTGCGAGTGCCTTAC 550
RESULT 13
AAQ06182
ID AAQ06182 standard; DNA; 696 BP.
XX
AC AAQ06182;
XX
DT 31-JAN-1991 (first entry)
XX
DE PR-1c cDNA cloned into plasmid pBSpr1-312.
XX
KW Transgenic plants; disease resistance; chimeric DNA;
  plant pathogenesis-related protein; ss.
XX
OS synthetic.
XX
FH Key Location/Qualifiers
FT mat_peptide 120..533
FT /tag= a
FT /product=PR-1c
XX
PN EP392225-A.
XX
PD 17-OCT-1990.
XX
PE 21-MAR-1990; 90BP-0105336.
XX
PR 20-OCT-1989; 89US-0425504.
PR 24-MAR-1989; 89US-0329018.
PR 20-JUN-1989; 89US-036672.
XX
PA (CIBA ) CIBA GEIGY AG.
XX
PI Ryals JA, Alexander DC, Goodman RM, Meins F, Payne GB;
PI Stinson JR, Neuhaus J-M, Moyer MB;
XX
DR WPI: 1990-313983/42.
DR P-PSDB; AAR08224.
XX
PT Disease-resistant transgenic plants - obtd. using encoding an
  inducible pathogenesis-related protein from infected plants.
XX
PS Example 15; page 24; 77pp; English.
XX
CC This chimeric DNA sequence comprises the PR-1c plant pathogenesis-
  related protein (PRP)-coding sequence (II), and a promoter sequence
  CC which enhances transcription of (II). This construct is used to
  CC produce transgenic plant cells or tissues with the ability to re-
  CC generate into plants which are disease resistant.
  CC See also AAQ06179-81, AAQ06183-86, AAQ06199-006208 and AAQ06829.
  CC
  XX
SQ Sequence 696 BP; 197 A; 140 C; 140 G; 219 T; 0 other;
Alignment Scores:
Pred. No.: 8,18e-13 Length: 696
Score: 296.00 Matches: 60
Percent Similarity: 55.88% Conservative: 16
Best Local Similarity: 44.12% Mismatches: 56
Query Match: 27.28% Indels: 4
DB: 11 Gaps: 2
US-09-832-320-2 (1-203) x AAQ06182 (1-696)
OY 69 GltTyrLeuAlaProHisGlnAlaArgAlaValGlyValAlaProLeuArgTyr 88
:::||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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DB 135 GACTATTTGGATGGCCATAACAGCTCGTCAGATGTAGGTGTAACCTTGCCTGG 194
OY 89 AsnAlaGlyLeuAlaSerAlaAlaAlaGlyThrValAlaGlnGlnArgGlnGly 108
DB 195 GAGCAGCAGGATGAGCGCTATGCAAAATATTCCTCCCAATGGCTGCAGATTGTAA 254
OY 109 CysAlaPheAlaAspValGlyAlaSerProTyrGlyAlaAsnGlnGlyTyrAlaSerTyr 128
DB 255 CTCGTACATTCACAT-----GTCACATGCGGAGAAACCTACCTTGGGAAAGTGC 305
OY 129 Arg---AlaArgProAlaGluValAlaLeuTyrValAlaGluGlyArgTyrTyrThr 147
DB 306 GATTCTTGGAGGCGCGTAAAGCGCTGAGATGTGGTCATGTAAGAAAGATTATGCC 365
OY 148 HisAlaAsnAsnThrCysAlaAlaGlyArgGlnCysGlyThrTyrGlnValAlaTyr 167
DB 366 CACGACTCAACACTTGTGCCCCAGACAGGTGTGGACACTATGCTCAGGTGGTGG 425
OY 168 ArgAsnThrAlaGluValGlyCysAlaGlnAlaSerCysAlaThrGlyAlaThrLeuThr 187
DB 426 CGTAACTCGCTTCGTTGATGTGCTAGGCTTCAGTGTACATGAGAGATATATGTC 485
OY 188 LeuCysLeuTyrAsnProHisGlyAsnValGlnGlyGlnSerProTyr 203
DB 486 TCTTGCACTATGATCTCCAGGTAATGTATAGCAGAAAGCCATAC 533
RESULT 14
AAV62807
ID AAV62807 standard; cDNA; 696 BP.
XX
AC AAV62807;
XX
DT 05-MAR-1999 (first entry)
XX
DE Tobacco PR-1c gene clone.
XX
KW Chemically regulatable DNA promoter; expression control; pesticide;
  herbicide tolerance; pathogenesis related gene; PR gene; ss.
XX
OS Nicotiana glauca.
XX
PN US5851766-A.
XX
PD 22-DEC-1998.
XX
PE 31-MAY-1995; 95US-0456262.
XX
PR 31-MAY-1995; 95US-0456262.
XX
PA (NOVUS ) NOVARTIS FINANCE CORP.
XX
PI Harms C, Ryals JA;
PI
XX
DR WPI: 1999-080396/07.
XX
PT Isolating chemically regulatable DNA sequences in plants - useful
  for chemically controlling expression in transformed plants
  CC
  XX
PS Example 44; Column 181-184; 175pp; English.
XX
CC This sequence represents a clone of the tobacco pathogenesis related (PR)
  CC gene. This gene can be isolated using the method of the invention.
  CC The method is for isolating a chemically regulatable DNA promoter
  CC fragment from the 5' flanking region of a chemically regulatable gene in
  CC a plant tissue. The method allows isolation of sequences which will be
  CC useful for the controlled expression of genes, under the control of a
  CC non-coding regulatable sequence. This is useful in plants with a
  CC herbicide or pesticide detoxification mechanism under the control of a
  CC chemical regulator, the regulator being applied before or with the
  CC herbicide or pesticide to give optimal tolerance. The promoter fragment
  CC is useful for controlling sequences which encode traits such as
  CC height, shape, development, male or female sterility, and the ability
  CC of the plant to withstand cold, heat, salt and drought. The chemical

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CC induction of the promoter allows the regulation of production of
 CC compounds, e.g. flavours, fragrances, pigments, natural sweeteners,
 CC industrial feedstocks, antimicrobials and pharmaceuticals, by
 CC biosynthesis or metabolite conversion, whose biosynthesis is controlled
 CC by endogenous or foreign genes. The method allows control over the time
 CC and rate of gene expression either throughout the whole plant, or in
 CC localized tissues, to achieve e.g. fungal or insect resistance by for
 CC instance dusting the leaves with the chemical regulator. Controlling the
 CC developmental processes by the application of a regulating chemical in
 CC e.g. the commercial production of cultivated crops allows processes such
 CC as germination, flower formation and fruit ripening to be synchronised at
 CC a given time.

XX Sequence 696 BP; 197 A; 140 C; 140 G; 219 T; 0 other;

Alignment Scores:

Pred. No.: 8,18e-13 Length: 696
 Score: 296.00 Matches: 60
 Percent Similarity: 55.88% Conservative: 16
 Best Local Similarity: 44.12% Mismatches: 56
 Query Match: 27.28% Indels: 4
 DB: Gaps: 2

US-09-832-320-2 (1-203) x AAV62807 (1-696)

OY 69 GUTYRLEUALAPROHISASNGIALAARGALAAVALAGLYVALAProLeuAArgTrp 88
 DB 135 GACTATTGGATGGCCATTAACACAGCTCGGAGATGTGTGGAACCTTTGACCTGG 194
 OY 89 AsnAlaGlyLeuAlaSerAlaAlaAlaGlyThrValAlaGlnGlnArgGlnGly 108
 DB 195 GAGCGCCAGGTAGCAGCTGATGCAAAATTAATGCTCCCAATGGCTGAGATTGTAC 254
 OY 109 CysAlaIleAlaAspValAGlyAlaSerProTyrGlyAlaAsnGlnGlyTyrAlaSerTyr 128
 DB 255 CTCGACATTTTCAT-----GGTCATACGGCGCAAAACCTAGCTTGGGAAAGTGGC 305
 OY 129 Arg---AlaArgProAlaGluValAlaAlaLeuTyrValAlaGlnGlyArgTyrTyrThr 147
 DB 306 GATTTCCTTGAGCGCGCTAAGGCCGTGAGATGTGGTCAATGAGAAACAGTATTATGCC 365
 OY 148 HisAlaAsnAsnThrCysAlaAlaGlyArgGlnCysGlyThrTyrThrGlnValAlaTrp 167
 DB 366 CACGACTCAAAACACTTGTGCCCAGACAGACAGGTGTGGACACTATACAGGTGGTTGG 425
 OY 168 ArgAsnThrAlaGluValAGlyCysAlaGlnAlaSerCysAlaThrGlyAlaThrLeuThr 187
 DB 426 CGTAACTCGGTTCGTGTGATGTGCTAGCGCTTCACTGTGACAAATGAGAGATATATTGTC 485
 OY 188 LeuCysLeuTyrAsnProHisGlyAsnValAGlnGlyGlnSerProTyr 203
 DB 486 TCTTCCACACTATGATCTCCAGGTAAATGATTATAGGCCAAAGCCCATAC 533

RESULT 15

AAV72999 standard; cDNA; 696 BP.

AAV72999;

25-FEB-1999 (first entry)

PR-1c protein encoding cDNA sequence.

Regulation; transcription; plant tissue; chimeric construction; PR;
 pathogenesis-related protein; anti-pathogenic; transgenic plant;
 beta-1,3-glucanase activity; pest resistance; ss.

Nicotiana sp.

US5847258-A.

08-DEC-1998.

PF 31-MAY-1995; 95US-0457364.
 XX 31-MAY-1995; 95US-0457364.
 PR 06-MAR-1988; 88US-0165667.
 PR 06-FEB-1989; 89US-0305566.
 PR 24-MAR-1989; 89US-0329018.
 PR 20-JUN-1989; 89US-0368672.
 PR 20-OCT-1989; 89US-0425504.
 PR 07-SEP-1990; 90US-0580431.
 PR 21-DEC-1990; 90US-0632441.
 PR 01-APR-1991; 91US-0678378.
 PR 27-SEP-1991; 91US-0768122.
 PR 06-MAR-1992; 92US-0848506.
 PR 06-NOV-1992; 92US-0973197.
 PR 06-APR-1993; 93US-0042847.
 PR 12-APR-1993; 93US-0045957.
 PR 16-JUL-1993; 93US-0093301.
 PR 13-JAN-1994; 94US-0181271.

PA (NOVS) NOVARTIS FINANCE CORP.

PI Moyer MB, Payne GB, Ryals JA, Ward ER;

WPI; 1999-059180/05.

PT DNA encoding pathogenesis-related glucanase proteins - useful for
 producing transgenic plants with enhanced disease or pest resistance

XX Example 44; Column 177-178; 169pp; English.

PS The present invention describes a DNA molecule encoding a
 CC pathogenesis-related (PR) protein having beta-1,3-glucanase activity
 CC selected from PR-2, PR-2', PR-N, PR-O and PR-O'. Also described
 CC are: (i) a chimeric gene comprising the above DNA molecule linked to a
 CC heterologous promoter; (ii) a vector containing the chimeric gene;
 CC (iii) a host cell containing the chimeric gene; (iv) a transgenic plant
 CC containing the chimeric gene; and (v) a seed from the transgenic plant.
 CC The DNA molecule is used to produce transgenic plants with enhanced
 CC disease or pest resistance. The present sequence represents a tobacco
 CC PR-1c protein encoding cDNA sequence from the present invention.

XX SQ Sequence 696 BP; 197 A; 140 C; 140 G; 219 T; 0 other;

Alignment Scores:

Pred. No.: 8,18e-13 Length: 696
 Score: 296.00 Matches: 60
 Percent Similarity: 55.88% Conservative: 16
 Best Local Similarity: 44.12% Mismatches: 56
 Query Match: 27.28% Indels: 4
 DB: Gaps: 2

US-09-832-320-2 (1-203) x AAV72999 (1-696)

OY 69 GUTYRLEUALAPROHISASNGIALAARGALAAVALAGLYVALAProLeuAArgTrp 88
 DB 135 GACTATTGGATGGCCATTAACACAGCTCGGAGATGTGTGGAACCTTTGACCTGG 194
 OY 89 AsnAlaGlyLeuAlaSerAlaAlaAlaGlyThrValAlaGlnGlnArgGlnGly 108
 DB 195 GAGCGCCAGGTAGCAGCTGATGCAAAATTAATGCTCCCAATGGCTGAGATTGTAC 254
 OY 109 CysAlaIleAlaAspValAGlyAlaSerProTyrGlyAlaAsnGlnGlyTyrAlaSerTyr 128
 DB 255 CTCGACATTTTCAN-----GGTCATACGGCGCAAAACCTAGCTTGGGAAAGTGGC 305
 OY 129 Arg---AlaArgProAlaGluValAlaAlaLeuTyrValAlaGlnGlyArgTyrTyrThr 147
 DB 306 GATTTCCTTGAGCGCGCTAAGGCCGTGAGATGTGGTCAATGAGAAACAGTATTATGCC 365
 OY 148 HisAlaAsnAsnThrCysAlaAlaGlyArgGlnCysGlyThrTyrThrGlnValAlaTrp 167
 DB 366 CACGACTCAAAACACTTGTGCCCAGACAGGTGTGGACACTATACAGGTGGTTGG 425

Oy 168 ArgAsnThrAlaGluValGlyCysAlaGlnAlaSerCysAlaThrGlyAlaThrLeuPhe 187
|||::: |||::: |||:::
Db 426 CGTAACTCGGTTCGTGGATGTCTAGGCTCAGTGTACATGAGATATATGTC 485
Oy 188 LeuCysLeuTyrAsnProHisGlyAsnValGlnGlyGlnSerProTyr 203
|||::: |||::: |||:::
Db 486 TCTTGCAACTATGATCCTCCAGGTAAAGTTATAGCAAAAGCCCATAC 533

Search completed: February 22, 2003, 03:07:51
Job time : 235 secs

10

11

12

13

GenCore version 5.1.4.p5.4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 22, 2003, 02:55:36 : Search time 1470 Seconds

(without alignments)
2236.520 Million cell updates/sec

Title: US-09-832-320-2

Perfect score: 1085

Sequence: 1 MAHSSHHHLLLPAPMATA.....ATLTLCLYPHGNVQGSPPY 203

Scoring table: BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:
-MODEL=frame+ p2n.model -DEV=xlp
-O=/gen2.1/USPTO.spool/US0983320/runat.20022003.092737.14802/app.query.fasta.1.391
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-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS-human40.cdi -LIST=45
-DOCALLIGN=200 -THR_SCORE=pcr -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFM=pic -NOR=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US0983320.0CGN.1.1.2874.0unal.20022003.092737.14802 -NCPU=6 -ICPU=3
-NO_XLPPY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -GAPOP=10 -XGAPEXT=0.5 -Fgapop=6 -FGAPEXT=7
-YGAOP=10 -YGAPEXT=0.5 -DELop=6 -DELEXT=7

Database:

EST.*
1: em_estba.*
2: em_esthum.*
3: em_estin.*
4: em_estnu.*
5: em_estov.*
6: em_estpl.*
7: em_estro.*
8: em_hic.*
9: gb_est1.*
10: gb_est2.*
11: gb_hic.*
12: gb_est3.*
13: gb_est4.*
14: gb_est5.*
15: em_estfun.*
16: em_estom.*
17: gb_gss.*
18: em_gss_hum.*
19: em_gss_inv.*
20: em_gss_pln.*
21: em_gss_vrt.*
22: em_gss_fun.*
23: em_gss_mam.*
24: em_gss_mus.*
25: em_gss_other.*
26: em_gss_pro.*
27: em_gss_tod.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	639	58.9	996	12	BG343299
2	568	52.4	362	13	BM101325
3	411.5	37.9	681	9	AU082529
4	402	35.7	666	13	BM259813
5	387.5	35.7	682	14	BQ411000
6	384	35.4	640	14	BQ010347
7	384	35.4	655	14	BQ015216
8	384	35.4	657	14	BQ011556
9	384	35.4	657	14	BQ013102
10	384	35.4	729	14	BQ986980
11	382	35.2	653	14	BQ013031
12	382	35.2	656	14	BQ013525
13	381.5	35.2	563	9	AT731816
14	380.5	35.1	637	12	BF268400
15	380	35.0	607	14	U47093
16	367.5	33.9	607	10	AM094514
17	366	33.7	653	14	BQ114041
18	364	33.5	639	14	BQ114394
19	363	33.5	551	9	AU497996
20	358	33.0	500	14	BQ252852
21	355	32.7	489	14	BQ114395
22	349.5	32.2	621	14	BQ411001
23	349	32.2	706	13	B1310259
24	348.5	32.1	628	10	AV782649
25	348.5	32.1	673	10	AV822028
26	346	31.9	660	14	BM813422
27	342	31.5	427	12	BG451575
28	342	31.5	486	10	BE512404
29	340.5	31.4	553	12	BG442275
30	337	31.1	634	10	BE600449
31	337	31.1	637	10	BE367243
32	337	31.1	759	11	AV106735
33	336.5	31.0	740	10	BE034124
34	333.5	30.7	554	10	AM037477
35	328	30.2	453	14	BQ114042
36	328	30.2	539	10	AM678619
37	328	30.2	588	10	BE597194
38	328	30.2	593	10	AM678759
39	328	30.2	611	10	BE367671
40	327	30.1	293	9	AU029886
41	325.5	30.0	578	13	B1124974
42	321.5	29.6	556	13	B1180121
43	320.5	29.5	752	17	BH449303
44	320	29.5	539	10	BE367566
45	320	29.5	554	10	AM746957

ALIGNMENTS

RESULT 1
BG343299
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE

996 bp mRNA linear EST 22-OCT-2001
HVSMSG0005F16f Hordeum vulgare pre-anthesis spike EST library
HYSDNA0008 (white to yellow anther) Hordeum vulgare cDNA clone
HVSMSG0005F16f, mRNA sequence.
BG343299
BG343299.1 GI:13155628
EST.
Hordeum vulgare.
Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae
; Triticeae; Hordeum.
1 (bases 1 to 996)

/cultivar="Nipponbare"

on obtaining a clone please contact: Martin Freyene

REFERENCE	TITLE	JOURNAL	COMMENT
127	SetYrArgAla-a---	ArgProLacIuValValAlaLeuTrpValAlaGlnGlyArgYr	145
319	AGCGAGCGCGCGGTACGCGCGTCTACGCGGTGGAAACTTGGGTAAAGAAAGAACTTAT		378
QY	146	TyTThHisAlaAsnThrCysAlaAlaIaGlyArgGlnGlySerGlyThrTyTThGlnVal	165
Db	379	TATGATTAATGGGACATTAATCTGGACCGGACATCATTAATGCTGTATATACAAAGTT	438
QY	166	ValTPRGAstnThrAlaGluValGlyCysAlaGlnAlaSerCysAlaThrGlnAlaThr	185
Db	439	GTTTGGAGAAATCTTCGGATTTGGGTTGCTGCACACGCTACATGCAAGATCAACTTACT	498
QY	186	LeuTrhLeuCysLeuTyTrAsnProHisGlnValGlnGlyGlnSerProTyR	203
Db	499	TTACATATTGTTTATATATCTCTCTGGTATTAATTAATTAAGGTGAGAAACCATAC	552
RESULT 6	BU010347	640 bp	MRNA linear EST 22-AUG-2002
LOCUS	OGJ13C16.yg.ab1	OG.EFGHJ	lettuce serriola
DEFINITION	OGJ13C16, mRNA sequence.		Lactuca sativa cDNA clone
ACCESSION	BU010347		
VERSION	BU010347.1	GI:22444742	
KEYWORDS	EST.		
SOURCE	Lactuca sativa.		
ORGANISM	Lactuca sativa		
REFERENCE	Kozlik,R.A., Michelnore,R.W., Knapp,S., Matvienko,M., Riseberg,L., Lin,H., van Damme,M., Lavelle,D., Chevallier,P., Ziegler,J., Ellison,P., Kolkmann,J., Slabaugh,M.S., Livingston,K., Zhou,Y., Dai,Z., Church,S., Jackson,L. and Bradford,K. lettuce and Sunflower ESTs from the Compositae Genome Project		
AUTHORS	http://compgenomics.ucdavis.edu/unpublished (2002)		
JOURNAL	Contact: Alexander Kozlik [R.W.Michelnore]		
COMMENT	Department of Vegetable Crops, R.W.Michelnore Lab		
	University of California at Davis (UCD)		
	Amundson Hall, UCD, Davis, CA 95616, USA		
	Tel: 1-(530)-742-1742		
	Fax: 1-(530)-752-9659		
	Email: akozlik@ucdavis.edu [michelnore@vegmail.ucdavis.edu]		
	belongs to contig OG_CA_Conf198161, see http://cgdb.ucdavis.edu/for details.		
	Plate: OGJ13 row: C column: 16.		
FEATURES	Location/Qualifiers		
source	1..640		
	/organism="Lactuca sativa"		
	/cultivar="L.seriola"		
	/db_xref="taxon:4236"		
	/clone="OGJ13C16"		
	/clone_lib="OG.EFGHJ lettuce serriola"		
	/lab_host="E.coli"		
	/note="Vector: pRCDNA5f1AB: The library was constructed from 10 different sources of RNA from a single genotype. Separate cDNAs were generated using primers that incorporated unique 5' and 3' tags to distinguish each source of RNA. cDNAs were then pooled, size-fractionated, directionally cloned into a custom medium-copy vector and transformations made with four size classes to minimize size bias. Details of each source of RNA and library construction can be obtained at http://cgdb.ucdavis.edu/RAG_LIB-OG.EFGHJ lettuce serriola		
	RAG TISSUE=flowers pre-fertilized		
	TAG_SEQ=CGTTGACGGG"		
BASE COUNT	167 a	133 c	178 g
ORIGIN			162 t

Pred. No.:	9,95e-26	Length:	640
Score:	384.00	Matches:	84
Percent Similarity:	55.56%	Conservative:	21
Best Local Similarity:	44.44%	Mismatches:	60
Query Match:	35.39%	Indels:	24
DB:	14	Gaps:	4

US-09-832-320-2 (1-203) x BU010347 (1-640)

OY	17	MelAtPvAlAcysLeuSerLeuAlaThrLeuLeuAlaLeuCysAlaAlaProAlaPro	36
Dd	11	ATGCAACAAAGCGTTCTTGTGGTCTTCACACTACTAGTAATGCCGCCACCCGACAAGACCGC	70
OY	37	ThnHisLcylValArgValLeuMetProCylcylValAclValAlaValThrTysAlaInGln	56
Dd	71	CCG-----GCGCGGGTGCGCCGCCGACGCACGGA-----	103
OY	57	GlyCylYThrClYserGlYserAsnAlaThrAlaSprCluYrTleuAlaProHisAsnGln	76
Dd	104	-----TATCTTAGAGCTCACACAAA	124
OY	77	AlaArgAlaAlaValGlyValAlaProLeuArgTrpAsnAlaGlyLeuAlaSerAlaIala	96
Dd	125	GCAAGAGCCGACGCTGGTGGTGGCTCCACTCAAGTGAACATCCAGCTCGGTAAAGCCACG	184
OY	97	AlaGlYThrValAlaGlnGlnArgArgGlnGlyCysAlaPheAlaAspValGlyIala	116
Dd	185	AGCTACTGGTGGCATTTACAGAGNAATGCANAAACTCCAGTTTGGCAACTTAACAGAC	244
OY	117	SerProTyrGlyAlaAsnGlnCylTrpAlaSerTYraG--AlaArgProAlaGluVal	135
Dd	245	GCGAAGTACGCGCGAAACCAATGtGGGCCACC GGCTGA GGTGTGACCCCGCGAGCGGTG	304
OY	136	ValAlaLeuTrpValAlaGlnGlyArgTYrTYrThrHisAlaAsnAsnThrCysAlaAla	155
Dd	305	GTCACAACTGGGTCTCGGAGAAGACGATTACACTTACGCCAATATTCATGTGCACCT	364
OY	156	GlyArgGlnCysGlyThrTYrThrGlnValValTTPatGAsnThrAlaGluValGlyCys	175
Dd	365	AGGCACCGGGTGGGTGTACACGAGGGGTGGCGGAACCTGGGGAGCGTGGGCTGT	424
OY	176	AlaGlnAlaSerGlyAlaThrGly--AlaThrLeuThrThrCysLeuTYraSProHis	194
Dd	425	GCTTGGCTAGGTGTCTTAAGATGCATCACTTACGCGATTTCTTTATTCCTCG	484
OY	195	GlyAsnValGlnGlnSerProTYr	203
Dd	485	GCGAATGTGATCGGAGAAGCCCTTAT	511
RESULT 7	BU015216	655 bp	mRNA linear EST 22-AUG-2002
LOCUS	BU015216		
DEFINITION	OGJ9J11.yg.abl.GG.ERHGJ lettuce seriola Lactuca sativa cDNA clone		
ACCESSION	OGJ9J11		mRNA sequence.
VERSION	BU015216		
KEYWORDS	BU015216.1 GI:22449611		
SOURCE	EST.		
ORGANISM	Lactuca sativa.		
REFERENCE	1 (bases 1 to 655)		
AUTHORS	Kozik,A., Michelmore,R.W., Knapp,S., Matvienko,M., Rieseberg,L., Lin,H., van Damme,M., Lavelle,D., Chevalier,P., Ziegler,J., Ellison,P., Kolkman,J., Slabaugh,M.S., Livingston,K., Zhou,Y., Lai,Z., Church,S., Jackson,L. and Bradford,K.		
TITLE	lettuce and sunflower ESTs from the Compositae genome project http://compgenomics.ucdavis.edu/ Unpublished (2002)		
JOURNAL	Department of Vegetable Crops, R.W.Michelmore lab		
COMMENT			

FEATURES	RESULT 9
LOCUS	BU013102
DEFINITION	BU013102 657 bp mRNA linear EST 22-AUG-2001
ACCESSION	OGJ3124.yg_ab1 OG_EFGHU lettuce serricola Lactuca sativa cDNA clone
VERSION	OGJ3124 mRNA sequence.
KEYWORDS	BU013102
SOURCE	BU013102.1 GI:22447497
ORGANISM	EST.
	Lactuca sativa.
	Lactuca sativa
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
	Asteridae; euasterids II; Asterales; Asteraceae; Lactuceae;
	Lactuca.
REFERENCE	1 (Bases 1 to 657)
AUTHORS	Kozik A., Michelmore R.W., Knapp S., Matvienko M., Riseberg L., Lin H., van Damme M., Lavelle D., Chevalier P., Ziegler J., Ellison P., Kolmann J., Slabaugh M.S., Livingston K., Zhou Y., Dai Z., Church S., Jackson L. and Bradford R. Lettuce and Sunflower ESTs from the Compositae Genome Project http://comgenomics.ucdavis.edu/unpublished (2002)
JOURNAL	Contact: Alexander Kozik (R.W.Michelmore)
COMMENT	Department of Vegetable Crops, R.W.Michelmore Lab University of California at Davis (UCD) Asmundson Hall, UCD, Davis, CA 95616, USA Tel: 1-(530)-742-1742 Fax: 1-(530)-752-9659 Email: akozika@ucdavis.org [michelmore@ucdavis.edu] belongs to contig OG_CA.Contig8161, see http://cgdb.ucdavis.edu/ for details. Plate: OGJ3 row: L column: 24.
	Location/Qualifiers

[illegible]

D_B 185 AGCTTACGTGTCGATTTCCAGAGATCGACAATAAAGCCAGTTTGCCAACTTAACGAAC 244
QY 117 SerProTyGlyAlaAsnGlnGlyThrIlePrpHisLeuArg---AlaArgProIleGluVal 135
D_B 245 GGGAGTAGCAGCGCGAANCCAGATGTGGGCCACCAGTGGGTGGTGCACCGCCAGACGCGTG 304
QY 136 ValAlaLeuTrpValAlaGlnGluLysArgTyrThrHisAlaAsnThrCysAlaAla 155
D_B 305 GTCCAGAACACTGGGTCTCGAGAGAAGCGATTATACCTTACCCCAATATCATGTGCACCT 364
QY 156 GlyArgGlnCysGlyThrTrhrcIleValValAlaPrpArgAsnThrIleGluValGlyCys 175、
D_B 365 AGCCACCGGGTGTGGGTGTACACGCAAGGGTGGTGGGAGACTCGGGCGAGCTGGGCTCT 424
QY 176 AlaGlnAlaSerCysAlaThrGly---AlaThrLeuThrIleuCysLeuTrpAsnProHis 194
D_B 425 GCATTGGCTAGGGTCTCTAAAGATCAAGCAACTTAAAGCATTTGCTTTTATCTCCTCG 484
QY 195 GlyAsnValGlnGlyInSerProTyr 203
D_B 485 GGGAATGTGATCGGAGAAAAGCCCTTAT 511

RESULT 13	LOCUS	DEFINITION
At7g3816	563 bp mRNA	linear EST 11-JUN-1999
At7g3816	563 bp mRNA	linear EST 11-JUN-1999
BMG5110971	Six-day Cotton fiber Gossypium hirsutum cDNA 5' similar to STS14 PROTEIN PRECURSOR, mRNA sequence.	similar

REVISION	AI731816.1	GI:5050668
KEYWORDS	EST.	
SOURCE	upland cotton.	
ORGANISM	Gossypium hirsutum	

ORGANISM
Gossypium hirsutum
Eukaryotes: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eucotsids II; Malvales; Malvaceae; Gossypium.
1 (bases 1 to 563)
Blewitt,M., Matz,E.C., Davy,D.F., and Burr,B.
ESTs from developing cotton fiber
Unpublished (1999)
COMMENT
Contact: Ben Burr

Brookhaven National Laboratory
Upton, NY 11973, USA
Tel.: 516-344-3396
Fax: 516-344-3407
Email: burr@bnl.bnl.gov
Seq primer: T3 Primer.

FEATURES	Location/Qualifiers
source	1. .563

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/organism="Gossypium hirsutum"
/cultivar="Acala Maxxa"
/db_xref="taxon:3635"
/clone_id="Six-day Cotton fiber"
/fibre_type="immature fiber"
/dev_stage="Six days post anthesis"
/lab_host="XL1-blue"
/notes="vector: pBluescript II KS+"

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Alignment Scores:	
Pred. No.:	1.42e-25
Score:	381.50
Percent Similarity:	54.08%
Best Local Similarity:	41.33%
Query Match:	35.16%
DB:	9
Length:	563
Matches:	81
Conservative:	25
Mismatches:	63
Indels:	27
Gaps:	4

US-09-832-320-2 (1-203) x A1731816 (1-563)

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Qy 16 PrometalaThraIaCysIeuLeuEuaIaThrLeuEuaIaIeu----- 30
    ||| ||::: |||||:::
Db 6 CCCAAATGGCCCTACGCCCTTGATTTACAATTCTACTCTAGACCAFTTACCAACACACAGGCC 65

```

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Oy 31 ---GysalalalProlaPro---ThrhiscgllyalArvalyLeumetProoglyGlyala 48
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Db 66 CMAAGTCGACGACACACACACGACACACACAGCTCCACCATCATGTGTGCA----- 116
Oy 49 GlyAlaValThrLySaInclngInclnglyThrlySerlySerSaInlaThrAlaasp 68
      |||
Db 117 -----CCAGCAGCCACA 128
Oy 69 GluTyRleuAlaProHisasnGlnAlaArgAlaAlaValGlyAlaAlaProleuA-Grtp 88
      :||| ||||| |||||
Db 129 GACTTCCTCCAAACCCACCAACCAACCAAGAGCTGCAGTAGGTGTGGCAGCTCCAAATGG 188
Oy 89 AsnAlaGlyLeuAlaSerAlaAlaAlaGlyThrValAlaInclngInlaArgArgInclngly 108
      :||| ||||| :|||
Db 189 AGCCAAACAATTACCAATGCTTCAAGTCATCGCAAGGTACCAADAGAACAAATAGGCT 248
Oy 109 CysAlaAlaAlaAlaAlaGlyAlaSerProtyrGlyAlaAsnGInclnglyTPAlaSerTyR 128
      ||| ||||| |||||
Db 249 TGTAGTGTGCACAACTGCACAAACCAAGTACGAGACAAACCGATTATGGGTACCGCA 308
Oy 129 ArgAla---ArgProAlaGluValAlaAlaLeuTyPAlaAlaGluGlyArgTyR 147
      ||| ||| ||| ||||| |||
Db 309 GCCCCCTCGACGCGCGTCATGCGCGGAGAACTGGCAAAAAGAAAGTAATTTWTGAT 368
Oy 148 HisAlaAsnAsnThrCysAlaAlaInclArgInclnglyThrTyRThrGlnAlaValTP 167
      :||| ||||| |||||
Db 369 TATGGACATAACTTGTGTGACCGGATCATTAATGTGTGTATTACTCAAGTTGTTGG 428
Oy 168 ArgAsnThrAlaGluAlaGlyCysAlaGlnAlaAserCysAlaThrGlyAlaThrleuTP 187
      :||| ||||| |||||
Db 429 AAGAAATCTTCGGATTGGTTCCTGCACAAAGTACATCAACAGATCAAGTTACTTTAACT 488
Oy 188 LeuCysLeuTyRAsnProHisGlyAsnValGInclngInserProtyR 203
      :||| ||||| |||||
Db 489 ATTTGTTTTATATCTCTCGTAATTATATAGGTGGAACCATCAT 536

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LOCUS	Bf266400	637 bp	MRNA	linear	EST 07-MAR-2001
DEFINITION	GA_EB0001103f Gossypium arboreum 7-10 dpa fiber library Gossypium				
	arborescens cDNA clone GA_EB0001103f, mRNA sequence.				
ACCESSION	Bf266400				
VERSION	Bf266400.1	GI:1199395			

[illegible]

REFERENCE
1 (bases 1 to 637)

AUTHORS Wing, R.A., Frisch, D., Yu, Y., Mein, D., Rambo, T., Simmons, J., Henry
D., Wood, T.C., Leslie, A. and Wilkins, T.A.
TITLE An integrated analysis of the genetics, development, and evolution
of the cotton fiber
JOURNAL unpublished (2000)
COMMENT Contact: Wing RA

Clemson University Genomics Institute
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwangel@clemson.edu
Seq primer: TATATGACATCACTATAGGG
High quality sequence stop: 629.
location/Qualifiers
1. 637

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/organism="Gossypium arboreum"
/strain="AKA"
/cultivar="8400"
/db_xref="taxon:29729"
/clone="GA_Eb0001L03f"
/clone_lib="Gossypium arboreum 7-10 dpa fiber library"

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Mon Feb 24 10:46:13 2003

us-09-832-320-2.p2n.rst

Page 12

Search completed: February 22, 2003, 04:05:00
Job time : 1489 secs

GenCore version 5.1.4.p5.4578
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OM protein - nucleic search, using frame_plus.p2n model

Run on: February 22, 2003, 02:08:51 ; Search time 1917 Seconds
(without alignments)

3081.831 Million cell updates/sec

Title: US-09-832-320-2

Perfect score: 1085
Sequence: 1 MAHRSHHLLLPAPMATA.....ATLTLCLYNEHGVQSQSPY 203

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2054640 segs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-DB=genmb1 -GEMT=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALLIGN=200 -THR_SCORE=pcr -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NOR=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09833320.cgn2_1.3745@runat_20022003_092737_14791 -NCPU=6 -ICPU=3
-NO_XLPHY -NO_MMAP -LARGEORDER -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=5 -DELOP=6 -DELOP=6 -DELOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELOP=6 -DELOP=6 -FGAPEXT=7

Database:

Genmb1:*
1: gb_ba:*
2: gb_hlg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_una:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pal:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*

29: em_vl:*
30: em_hlg_hum:*
31: em_hlg_inv:*
32: em_hlg_other:*
33: em_hlg_mus:*
34: em_hlg_pln:*
35: em_hlg_rtd:*
36: em_hlg_mam:*
37: em_hlg_vrt:*
38: em_ay:*
39: em_hgo_hum:*
40: em_hgo_mus:*
41: em_hgo_other:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	699.5	64.5	144573	2 AC096689	AC096689 Oryza sat
2	699.5	64.5	150928	2 AC103550	AC103550 Oryza sat
3	699.5	64.5	150928	2 AC103550	AC103550 Oryza sat
4	365.5	33.7	1340	8 STS14	STX2652 S. tuberosum
5	365.5	33.7	1340	8 STU17111	U17111 Solanum tub
6	348.5	32.1	585	8 AY093248	AY093248 Arabidops
7	348.5	32.1	585	8 AY093248	AY093248 Arabidops
8	348.5	32.1	585	8 AY093248	AY093248 Arabidops
9	347.5	32.0	683	8 AY086114	AY086114 Arabidops
10	347.5	32.0	683	8 AY086114	AY086114 Arabidops
11	347.5	32.0	683	8 AY086114	AY086114 Arabidops
12	347.5	32.0	683	8 AY086114	AY086114 Arabidops
13	347.5	32.0	683	8 AY086114	AY086114 Arabidops
14	347.5	32.0	683	8 AY086114	AY086114 Arabidops
15	347.5	32.0	683	8 AY086114	AY086114 Arabidops
16	347.5	32.0	683	8 AY086114	AY086114 Arabidops
17	347.5	32.0	683	8 AY086114	AY086114 Arabidops
18	347.5	32.0	683	8 AY086114	AY086114 Arabidops
19	347.5	32.0	683	8 AY086114	AY086114 Arabidops
20	347.5	32.0	683	8 AY086114	AY086114 Arabidops
21	347.5	32.0	683	8 AY086114	AY086114 Arabidops
22	347.5	32.0	683	8 AY086114	AY086114 Arabidops
23	347.5	32.0	683	8 AY086114	AY086114 Arabidops
24	347.5	32.0	683	8 AY086114	AY086114 Arabidops
25	347.5	32.0	683	8 AY086114	AY086114 Arabidops
26	347.5	32.0	683	8 AY086114	AY086114 Arabidops
27	347.5	32.0	683	8 AY086114	AY086114 Arabidops
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29	347.5	32.0	683	8 AY086114	AY086114 Arabidops
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31	347.5	32.0	683	8 AY086114	AY086114 Arabidops
32	347.5	32.0	683	8 AY086114	AY086114 Arabidops
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35	347.5	32.0	683	8 AY086114	AY086114 Arabidops
36	347.5	32.0	683	8 AY086114	AY086114 Arabidops
37	347.5	32.0	683	8 AY086114	AY086114 Arabidops
38	347.5	32.0	683	8 AY086114	AY086114 Arabidops
39	347.5	32.0	683	8 AY086114	AY086114 Arabidops
40	347.5	32.0	683	8 AY086114	AY086114 Arabidops
41	347.5	32.0	683	8 AY086114	AY086114 Arabidops
42	347.5	32.0	683	8 AY086114	AY086114 Arabidops
43	347.5	32.0	683	8 AY086114	AY086114 Arabidops
44	347.5	32.0	683	8 AY086114	AY086114 Arabidops
45	347.5	32.0	683	8 AY086114	AY086114 Arabidops

RESULT 1

ALIGNMENTS

[illegible][illegible]

DB 898 GGACAAACAAATTCGACCTTTCCTAATTAAAGTAATGCCAAATATGTCGCAATCAAT 957

OY 124 YTPPAlaSerTyrArg---AlaArgProAlaGluValAlaLeuTrpValAlaGlu 143

DB 958 ATGGGCTAGTGGACGGTGGTGCACCCAGCAATGGCTGCTGCTTGTGGTGTGAGAA 1017

OY 143 YARGTyrTyrThrHisAlaAsnThrCysAlaIaGlyArgGlnCysGlyTrpTyr 163

DB 1018 GAATTTTAACTATGAAATTAATTCATGTCACAGGGATGATAGTGGAGTTTATAC 1077

OY 163 TGLValValTrpArgAsnThrAlaGluValAlaGlyCysAlaGlnAlaSerCysAla 183

DB 1078 CCAATATGTTGGAAAGAAACAAATGAGATGGTGTGGACAGCTACTCTTTCGAGAG 1137

OY 183 Y---AlaThrLeuThrLeuCysLeuTyrAsnProHisGlyAsnValGlnGlyGlnSer 202

DB 1138 ACGTGCTACTTACTATGATGTTCTATATATCCACCTGGAAATGTAATGAGAGAAC 1197

OY 202 CTyr 203

DB 1198 TTAT 1201

RESULT 5

LOCUS AY093248

DEFINITION Arabidopsis thaliana unknown protein (At5g66590) mRNA, complete cds.

ACCESSION AY093248

VERSION M1093248.1 GI:20259799

KEYWORDS P11.CDNA.

SOURCE Arabidopsis thaliana.

ORGANISM Arabidopsis thaliana.

REFERENCE 1 (bases 1 to 585)

AUTHORS Southwick, A., Karlín-Neumann, G., Nguyen, M., Lam, B., Miranda, M., Palm, C. J., Chung, M. K., Hayashizaki, Y., Ishida, J., Kamiya, A., Kawai, J., Kim, C., Lin, J., Liu, S. X., Narusaka, M., Pham, P. K., Sakano, H., Sakurai, T., Satou, M., Seki, M., Shim, P., Yamada, K., Shinzaki, K., Becker, J., Theologis, A. and Davis, R. W.

TITLE Direct Submission

JOURNAL Submitted (26-MAR-2002) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304, USA

COMMENT e-mail for correspondence: arab@eesequence.stanford.edu

RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA: RIKEN Arabidopsis Full-Length cDNA): Seki, M., Narusaka, M., Ishida, J., Satou, M., Kamiya, A., Sakurai, T., Carninci, P., Kawai, J., Hayashizaki, Y. and Shinzaki, K.

The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAFL cDNAs: Southwick, A., Nguyen, M., Karlín-Neumann, G., Lam, B., Miranda, M., Palm, C. J., Bowser, L., Jones, T., Ban, J., Chen, H., Cheuk, R., Chung, M. K., Kim, C., Lin, J., Liu, S. X., Pham, P. K., Sakano, H., Shim, P., Yamada, K., Becker, J., Theologis, A. and Davis, R. W.

Southwick, A., (SSP/Stanford) and Seki, M. (RIKEN GSC) contributed equally to this work. Shinzaki, K. (RIKEN GSC) and Davis, R. W. (SSP/Stanford) contributed equally to this work as PIs.

location/Qualifiers

1. 585

/organism="Arabidopsis thaliana"

/db_xref="taxon:3702"

/chromosome="5"

/clone="U15768"

/note="This clone is in PENTR/SD-dtopo. This is a cloned PCR product using RIKEN clone RAFL04-20-B17 (AF386987) as a template

gene

ecotype: Columbia"

1. 585

/gene="At5g66590"

/note="K1F13.27"

1. 585

/gene="At5g66590"

/codon_start=1

/product="unknown protein"

/protein_id="AAK13247.1"

/db_xref="GI:20259800"

/translation="MAITTHIIFVALLVIVKRAISPAKIKRKQIVTSPPTISA

AAKATDANKRAKAVGVPPIVWSQITLKAASRLARYQNRKCEFAIINGKYGAND

LMAKGVAVTPSLAVETWKEPEYNNKSDTCANHTSCVYKQVYWRNSKEIGCAQNT

CKRSTVLTICFYNPENVGOKPY"

BASE COUNT 157 a 150 c 137 g 141 t

ORIGIN

Alignment Scores:

Pred. NO: 3.1e-13 Length: 585

Score: 348.50 Matches: 69

Percent Similarity: 60.14% Conservative: 17

Best Local Similarity: 48.25% Mismatches: 54

Query Match: 32.12% Indels: 3

DB: 8 Gaps: 2

US-09-832-320-2 (1-203) x AY093248 (1-585)

OY 64 AasnAlaThrAlaAspGluTyrLeuAlaProHisAsnGlnAlaArgAlaValGlyVal 83

DB 127 TCTGCAGCAGCTTAAGACCTTTCACCGATGCCCAACAGCCACAGCATGTTGCTT 186

OY 84 AlaProLeuArgTyrPaspAlaGlyLeuAlaSerAlaAlaAlaGlyThrValAlaGln 103

DB 187 CCACCACTTATGTTGAGCCAGACGTTGGAGAGTGGTGGATGCTGCTACAC 246

OY 104 ArgArgGlnGlyGlyCysAlaPheAlaAspValGlyAlaSerProTyrGlyAlaAsnGln 123

DB 247 AGGACCAAGAAAGAGTGTAGTTCGGAGCTTAAACCTGGAAATACGGCCACAG 306

OY 124 GlyTrpAlaSer-----TyrArgAlaArgProAlaGluValAlaAlaLeuTrpValAla 141

DB 307 CTTGGGCTTAAGGCTTACTAGACCGCTGACACCGTCTCTGCTGGAGACTGGGAG 366

OY 142 GlnGlyArgTyrTyrThrHisAlaAsnThrCysAlaIaGlyArgGlnCysGlyThr 161

DB 367 GAGAAACCTTCTACAAATATATAAGTCAGACAGTGTGCGAACCACACAGTGGG 426

OY 162 TyrThrGlnValValTrpArgAsnThrAlaGluValAlaGlyCysAlaGlnAlaSerCysAla 181

DB 427 TATTAACAGTCTGTGGAGAAACTCTAAAGAGCTCGGGTGTGCTCAAGCCAGCTG 486

OY 182 ThrGlyAlaThr---LeuThrLeuCysLeuTyrAsnProHisGlyAsnValGlnGlyGln 200

DB 487 AAAGAGTCACAGCGTGTGACCACTTGTTTTACAACTCTCTGGAATGTAAATGG 546

OY 201 SerProTyr 203

DB 547 AAGCTTAC 555

RESULT 6

LOCUS AF386987

DEFINITION Arabidopsis thaliana unknown protein (K1F13.27) mRNA, complete cds.

ACCESSION AF386987

VERSION M1093249

KEYWORDS P11.CDNA.

SOURCE Arabidopsis thaliana.

ORGANISM Arabidopsis thaliana.

REFERENCE 1 (bases 1 to 624)

AUTHORS Lam, B., Southwick, A., Karlín-Neumann, G., Nguyen, M., Miranda, M.,


```

Db 241 ACCGAG---AGGATCGGCGACTGCAGACTCCGAGC---GGGCTTCAGGGGAGA 294
OY 122 snngllytrpalaSerTyArgala-----ArgProAlaGluValAlaLeuTrpV 140
Db 295 ACATCTCTGGGTCGCGCGGCGGCGACTGCAGAGCGCGGACGGGTGAAGCTGTGG 354
OY 140 alalaglugllytrpThrHisAlaAsnThrCysAlaAlaAlaArgGlnCysG 160
Db 355 TGGACGAGAGAGAGACTACGACTACGGGTCCACACACTGTGCGAGGGGAGAGTGTGCG 414
OY 160 lyThrThrThrGlnValValTrpArgAsnThrAlaGluValGlyCysAlaAlaSerC 180
Db 415 GGCACCTACGACGAGTGTGGTGGCGGCTGCACGACGATCGGCTGCGCTGCTCT 474
OY 180 ys---AlaTrpGlyAlaThrLeuThrLeuCysLeuTyraAsnProHisGlyAsnValGln 199
Db 475 GCACGACGAGAGCGGCGGCTTCATCATCAGCTGCAGACTACGAGCCCGCGGAGATTTGTTG 534
OY 199 lyGlnSerProTyR 203
Db 535 GACGAGAACCATAC 548

RESULT 12
TIN24
LOCUS TIN24 127053 bp DNA linear PLN 21-JUN-1999
DEFINITION Arabidopsis thaliana BAC TIN24.
ACCESSION AF149413
VERSION AF149413.1 GI:4809270
KEYWORDS
SOURCE
ORGANISM
Arabidopsis thaliana.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 127053)
Washington University Genome Sequencing Center.
The A. thaliana Genome Sequencing Project
REFERENCE
1 Unpublished (1997)
JOURNAL
2 (bases 1 to 127053)
AUTHORS Murray, J., Langston, Y., Clarke, K. and Drone, K.
TITLE The sequence of A. thaliana TIN24
JOURNAL Unpublished (1999)
REFERENCE
3 (bases 1 to 127053)
AUTHORS Waterston, R.
TITLE Direct Submission
JOURNAL Submitted (10-MAY-1999) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
4 (bases 1 to 127053)
REFERENCE
4 (bases 1 to 127053)
AUTHORS Waterston, R.
TITLE Direct Submission
JOURNAL Submitted (21-JUN-1999) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
COMMENT
Genome Sequencing Center
Department of Genetics, Washington University,
St. Louis, MO 63108, USA
e-mail: twatson@wustl.edu

```

MAPING: Clones were assigned to the YAC map by hybridization by M. Lodhi, Cold Spring Harbor Laboratories, and fingerprinted by M. Marra, Washu, to pick the best candidates for sequencing.

NOTICE: This sequence may not be the entire insert of this clone. It may be shorter because we only sequence overlapping sections once, or longer because we provide a small overlap between neighboring submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded or sequenced with an alternate chemistry; an attempt was made to resolve all sequencing problems,

such as compressions and repeats; all regions were covered by sequence from more than one subclone

NEIGHBORING COSMID INFORMATION:

The 3' clone is F18A17. Actual start of this clone is at base position 1 of TIN24; actual end is at 127053 of TIN24

The 3' neighbor F18A17 was sequenced at the Lita Annenberg Hazen Genome Sequencing Center, Cold Spring Harbor Laboratory, ACCESSION # AC005405.

NOTES:

Coding sequences below are predicted from computer analysis, using the program GeneFinder (P. Green and L. Hillier, ms in preparation).

FEATURES

source

```

1..127053
/organism="Arabidopsis thaliana"
/cultivar="Columbia"
/db_xref="taxon:3702"
/chromosome="V"
/map="unknown"
/clone="TIN24"
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/gene="TIN24.15"
join(6032..6206,6502..6814,6901..7192,7282..7383,
7450..7878,7954..8670)

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CDS

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/gene="TIN24.15"
/note="contains similarity to protein kinase domains; Pfam
PF00069, score=129.3, E=7e-35, N=1"
/codon_start=1

```

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/evidence-not-experimental
/protein_id="AAD40140.1"
/db_xref="GI:5107827"

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/translacion="MASPYSSDDIHSPNVSTVAVIDEKHSYAVRWAVDHLNMIH
PMLIVHRTKNSNHDSDVAKTLDVYNNLVNVLVAGSTKTFARSMFSKPHVQ
SISMSSTDFCSYVYISKGGVGSRRPQKPIINTLAPRPSGFLIQLSDSDQD
IRVORSARNRPNETTYPHNPAANTPOKPKPIINGSDPNNNGNOAFOPILOS
SFSDSDGDFGMSGVLDLSSONSDYFHGASSSESIPOSTRDIEAEERLKEIKO
TMDVYSACKEALTAARKANELNOMKTEEARERKARLESEAAALVATIERAKOCTN
EAAERKQMAELEGGRRKQAEKAVSEKQDRKAVSALAHNDVRYRKYSEIEPEATE
RANRPRKIGRGGYGVYNGELDHPVAKVLPDPAAGKROQOQEVYLCSTRHHMY
LLGCGPEYCCIVFEFBNQSLERLRFRTGNSPFSWRKRFETAAELPAALSETLOAK
PEPLVHRODLKPAHLDLKNVSKISDVGLAKLPASIASVQFPHTSAGTFCYIDP
EYQNGMLTTSQSVYSIGILLQILITGRPPWGLAHQVSAISKGFKEMLDPVYDWP
VQDAQSFATLAKCAELKRDRLGKEVVPHLIRLKNFGNDGDERTEHMT"
/complement(14495..15335)
/gene="TIN24.16"
/complement(join(14495..14593,14673..14816,14910..14979,
15134..15240,15324..15335))
/gene="TIN24.16"

```

```

/note="contains similarity to a Saccharomyces cerevisiae
hypothetical protein (SW:P47044) and a Bacillus subtilis
hypothetical protein (GB:U15180)"
/codon_start=1

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/evidence-not-experimental
/protein_id="AAD40141.1"
/db_xref="GI:5107828"
/translacion="MTEHTISGEVGEVRIVSDMHRKATMAGAFATLIGERYE
MELEMTMTMOLGTHKKTVGLLNDGVYVNLAPFDVGESEFKQACNCTIVSAPS
AELEMKMEIYTPSHKTYASHQSKVPELDYDLNENKRPQ"
17527..18021
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17527..18021
/gene="TIN24.14"

```

```

/note="contains similarity to SCP-1-like extracellular
proteins; Pfam PF00188, score=196.7, E=3.7e-55, N=1"
/codon_start=1
/evidence-not-experimental
/protein_id="AAD40121.1"

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Genes were predicted from the integrated results of the following: GENSCAN1.0, BLASTN2.0, BLASTX2.0 as well as SplicePredictor (October 1998 version). The genomic sequence was searched against NCBI Nonredundant Protein database, nr (<ftp://ncbi.nlm.nih.gov/blast/db>) and the cDNA sequence database at RGP. Protein homologues of the coding regions were searched against NCBI Nonredundant Protein database with BLASTP2.0. ESTs representing the identified cDNA sequences using BLASTN 2.0 with the corresponding DBI accession no. and RGP clone ID.

A gene with identity or significant homology to a protein is classified based on the protein name to indicate the homology level such as same name, 'putative' and '-like protein'. A gene without significant homology to any protein but with EST homology (covering almost the entire length of partial sequence) is classified as an 'unknown' protein. A gene predicted with a gene prediction program is classified as a 'hypothetical' protein.

The orientation of the sequence is from -21M13 to M13rev of the BAC clone. Detailed information on overlap and assembly quality together with annotation of this entry is available at <http://rgp.dna.affrc.go.jp/genomeSeq.html>.

FEATURES

source

1. 155939
/organism="Oryza sativa (japonica cultivar-group)"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/chromosome="1"
/clone="OSJNBa0091E23"
complement(2830..6157)
/gene="OSJNBa0091E23.1"
complement(2830..6157)
/gene="OSJNBa0091E23.1"
/note="Probably inactive due to frameshift(s) in CDS
probably inactive due to stop codon(s) in CDS
pseudogene, TNP-like transposable element"
/pseudo
8140..8634
/gene="OSJNBa0091E23.2"
8140..8634
/gene="OSJNBa0091E23.2"
/codon_start=1
/product="Rice pathogenesis-related protein class 1"
/protein_id="BAB84468.1"
/db_xref="GI:18461272"
/translation="MEYSKRLATSLFVLAVAATMFCSDAONSPODYLRHNAARAVGCP
VTWDTVOAFAENTASQSGDCSLIHSSRNNGEMLTNGSGEDMTAASQVSGE
KSDYDASNSCAQKCGHYTYVMRASTIGCARVCSNGHVFITCNVPAQFEWG
QRPY"
join(11408..11439,14340..14529)
/gene="OSJNBa0091E23.3"
join(11408..11439,14340..14529)
/gene="OSJNBa0091E23.3"
/note="hypothetical protein"
/codon_start=1
/protein_id="BAB84469.1"
/db_xref="GI:18461273"
/translation="MGRGIIHGMRRRRRGAAGARRKPGAVGPMWVVASARGRRR
LRPPAGGGGGRPRRELGMIFSIFFFF"
complement(join(19031..19092,19181..19629,19712..19843,
20623..20627))
/gene="OSJNBa0091E23.4"
complement(join(19031..19092,19181..19629,19712..19843,
20623..20627))
/gene="OSJNBa0091E23.4"
/codon_start=1
/product="zeta1-COP like protein"
/protein_id="BAB84470.1"
/db_xref="GI:18461274"
/translation="MKSRPTPHITLKKRRSSASLSSSTSPVAVVVTTPAIVSE
SASPGTATPTPRSHRBSAASTIVYVPPPTSTSEAAASSSPOPIQASRTLA
GDVDSKEMASFLVRRSRISAVITIRCIQGEPLFSLIYTHLLDLTIVHCKQLI
VPPESSFTRGASPSRSTSHRCHODLNPSTHEPPLTALIGATPSSQEN"
join(22340..22759,25490..26449)
/gene="OSJNBa0091E23.5"

CDS

join(22340..22759,25490..26449)
/gene="OSJNBa0091E23.5"

/codon_start=1
/product="putative benzoyltransferase"
/protein_id="BAB84471.1"
/db_xref="GI:18461275"

/translation="MEIVGECIYNPNPVLVPSKPTPKALTYLSNLDORLHFPDIY
IYPTGDTLGDITKVALSVLVYVPLAGRLASNEHDKLIDCNSGVYFAEGFLP
GLTFGDTILGHAKPSMKRLYKIDQSVCTPPLVQVOTLISGDTILCGATAGVS
DAFAAHEFLAMARAMSDESELAHPVACDRALAPROTPRIAPAHPEALVAGG
DDAAVAHEASSRLPAPLPSVLTPTMAVATLKLVA.PSASPLECTSPREALAHY
RAVYRALDPPASLPILKLTPTMGIRLVRKELSGCYCNGVILACASTAGOLAAAP
DAALVETKORVDDVYNSVDLLEVRKGLPDLAFTTISLIRGLEDIDGEGT
PVHGPLTSVYCLFLPVIGDPGATALVSQAADSEFRCCHDGDVDDVEDKQDL
PNIDGNAS"
join(29342..29466,29780..29964,30172..30641)
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join(29342..29466,29780..29964,30172..30641)
/gene="OSJNBa0091E23.6"
/note="contains ESTs AU076106(E20423), AU081502(C10364)"
/codon_start=1
/product="retrotransposone gag-pol polyprotein-like"
/protein_id="BAB84472.1"
/db_xref="GI:18461276"

/translation="MSTDGGVNGGAVGCGGCGENDINGNNNSNISFGASSKP
SEPLSPKEAMFESADCLFHALISVLADNITLDVYMMPSKMDMDVAKPVSDA
KGFVTLTIGSLGVEEKVRAKNDPKITKRGSSANLVOKKPNAPHNNNKKVKKDVL
KATNFTKKKCKGKAGKNCPCYCSGMADCDPHDKRSANVISEGCTSGYKFLP
TVLSIFHSPDWYDTPFHRSRLRTLHGLTETGAVYARLK"
complement(32520..33023)
/gene="OSJNBa0091E23.7"
complement(32520..33023)
/gene="OSJNBa0091E23.7"
/note="contains EST AU070895(R10430)"
/codon_start=1
/product="putative pathogenesis-related protein precursor"
/protein_id="BAB84473.1"
/db_xref="GI:18461277"

/translation="MEASKRLATSLFVLAVAATMFCSDAONSPODYLRHNAARSA
VGVPMSWSTKLGFAEDYARORRQKDCRLQHSNGEINIGSGADMTAADVVRSM
VDKERYNYNASNSCAKVCGHYTYVMRDSTNVGCAARVCDAKNGFIITCNVPEGRN
IVGRPPY"
join(35671..35809,36942..36964)
/gene="OSJNBa0091E23.8"
join(35671..35809,36942..36964)
/gene="OSJNBa0091E23.8"
/note="hypothetical protein"
/codon_start=1
/protein_id="BAB84474.1"
/db_xref="GI:18461278"

gene

/translation="MGRRLPWCLEWGEDQEKDAAGSNRRRSDEGEAANAFDQK
RIGVNDLI"
complement(join(39777..40698,40725..41083))
/gene="OSJNBa0091E23.9"
complement(join(39777..40698,40725..41083))
/gene="OSJNBa0091E23.9"
/codon_start=1
/product="similar to Oryza sativa chromosome 1,
p045H0310.25"
/protein_id="BAB84475.1"
/db_xref="GI:18461279"

CDS

/translation="MKRKASSFSFGDPPASPTTVDSFCDDVIAEFLVRLPVSPL
ARAACAVKMRRAVSPALFRRHHLHQAPQLGHIYTYECSSRPVQAPPTSD
PELSAVRHGDFLPTVLPRLPPPEELRHQRELTVPVARRVLAFLTPPRGNR
AFHNHSGFLTIGRVGQOAASSSFVYVMORCSTTVIYASGDORLDMELAYDSS
TGANSARWNTSDIDMDPLIKYRSAMHAPRCLIKRAGSINSILVSLDATTMGS
PEVAPPPGVLLGFSYAVGDDDSMCLVNMHEGRWRLVLSKRWHLRWLLKSGC
GSAVAVLDDEGETSLTSTEDAADMLMDYDRCRYAVAVNAGVVLCLHSPRLNDRT
AFRLSNLEVYVSFASPPVQYOMPPLTPA"
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	Oy	20	-----Alaysteulemleumlaithrieulemlaleucys 31	
	Dy	154	NCAATGAGAGGCATCCACAACAGCTGCAGTCTTGCTCCTGTGGCTGCGTCAAGCAGCTGCC	213
	Oy	32	AlalaProLaiaProLathrHisGlYalaaRValleumetProglYelYalaglYalaaVal	51
	Dy	214	ACTGCGGTGACCCCTTCCTCAC-----	234
	Oy	52	ThrylYalagInglngInglYlThrGlYserGlYserAsnAlarHraalspGluYrIleu	71
	Dy	235	-----TCTGAATTTGCTCTCAAGACTACCTC	261
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	Dy	262	ACTCTCCAAAACGCCGCCCTCTCCCTCCCTGTGTGGCCCCGGACCTGACCAGCAAG	321
	Oy	92	LeuAlaSerAlaAlaAlaGlYThrValAlagIngnArgrgInglYelCySalaphe	111
	Dy	322	CCTGAGCAGTCTCCACAGAAGTACCCGCCAGG-----AGGGCCGGCGACTCCCTCTC	375
	Oy	112	AlaaspYalGlYAlaserProTrYGlyAlasngInglYTRP-----AlaserYrag	129
	Dy	376	CAGCAGCTCGGGC---GGGCCCTACGGGAGAAACATCTTCGTGGGGTCCCGCGCTTCAT	432
	Oy	130	AlaArgProLaiaGluaValAlaLeuTrPaValAlaGluglYarglYrYrThrHisAla	149
	Dy	433	TGGAGAGCGGTGACGCCCATGTGCATGTGCGTAAGCGAAMCAAGTGTCAACTACGCG	492
	Oy	150	AsnaAsnThrcysAlaAlaAlaGlYarGIngcylYsGlYThrTrhgInValYalTPraAsn	169
	Dy	493	ACCAACAGCTGCGCCGCCGCAAGGTGTGTGGCACTACACGAGGTGTGGCGCGCG	552
	Oy	170	ThralaGluaValGlYcysAlaInglAlaserCyAlaThrGly---AlaThrLeuThrLeu	188
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RESULT 15	AP004057	110235 bp	DNA linear HTG 21-MAR-2002	
LOCUS	Oryza sativa (japonica cultivar-group)	chromosome 2 clone		
DEFINITION	Oryza sativa E06, *** SEQUENCING IN PROGRESS ***, in ordered pieces.			
ACCESSION	AP004057			
VERSION	AP004057.1	G1:15208425		
KEYWORDS	HTGS-PHASE2.			
SOURCE	Oryza sativa (japonica cultivar-group) (cultivar:Niponbare)	DNA,		
ORGANISM	clone:OJ1316.E06.			
REFERENCE	1 Sasaki,T., Matsumoto,T. and Yano,M. R.			
AUTHORS	Oryza sativa niponbare(GA3) genomic DNA, chromosome 2, BAC			
TITLE	clone:OJ1316.E06			
JOURNAL	Published Only in Database (2001)			
REFERENCE	2 (bases 1 to 110235)			
AUTHORS	Sasaki,T., Matsumoto,T. and Yamamoto,K.			
TITLE	Direct Submission			
JOURNAL	Submitted (15-AUG-2001) Takuji Sasaki, National Institute of			
	Agrobiological Resources, Rice Genome Research Program, Kannondai			
	2-1-2, Tsukuba, Ibaraki 305-8602, Japan			
	(E-mail:tsesaki@affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/,			
	Tel.:81-298-38-7441, Fax:81-298-38-7468)			
	The nucleotide sequence of this BAC clone was generated by			
	combining Monsanto and Rgp-Japan sequencing data.			
COMMENT	NOTE: it currently consists of 1 contigs. Gaps between the conligs			

are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

*NOTE: This is a 'working draft' sequence.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

FEATURES	SOURCE	Location/Qualifiers
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BASE COUNT	30404 a	23562 c 24043 g 32226 t
ORIGIN		

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Pred. No.:	1.05e-08
Score:	110233
Percent Similarity:	38.00%
Best Local Similarity:	40.02%
Query Match:	42.08%
DB:	28.57%
Gaps:	2
Length:	110233
Matches:	85
Conservative:	12
Mismatches:	65
Indels:	40
Gaps:	10

US-09-832-320-2 (1-203) x AP004057 (1-110235)

QY	13	LeuProAlaProMetAlaPrrAlaCysLeuLeuAlaThrLeuLeuAlaLeuGlyAla	32
Db	54196	CTCCGCTTCCGGGGGCGACACGGCGGACGCCCTC	54233
QY	33	AlaProAlaProThrHisGlyAlaArgValLeuMetProGlyGlyAlaGlyAlaValThr	52
Db	54232	CTCCACGGCGGCC-----GCCGACGGCAAGGTGG	54258

53 LysAlaGlnGlyThrGlySerGlySerAsnAlaThrAlaAspGluTyrLeuAla 72

Db 54259 TCCTCGTCGTCGGGGAGACGAGAGC-----CTCGCGTCGGGGTCCCTGGAC 54306

cy / 3 P10H1SASHGlnAaTgAiaAaVaIGYvaLmaPtoLeuaTgtPrashAaGlyLeu 92

[illegible][illegible]

Over 112,000 people have been killed in the conflict.

Db 54427 GTGCAC---TCGCACGGGGCCGTACGGGGAACCTGTTCCACGGGCAAGGGCGTGGGTGG 54483

QY 126 ALaSeTyrArgAlaArgProAlaGluValValAlaLeuTrpValAlaGluGlyArg--- 144

Db 54484 GCG-----CCCGCGACGTGTTGGCGCGCTGGTGTCCGCGGAGCGCGG 54528

QY 145 TYR¹TYR²THR³ALA⁴ASN⁵THR⁶CYS⁷ALA⁸GLY⁹-----ARG¹⁰GLN¹¹CYS¹²GLY¹³THR¹⁴TYR¹⁵ 162

Db 54529 CTGTACGACGCGCGCTCCAACTCGTGCCGCGCGCGGACGCCGCGGTGCGGGCACTAC 54588

163 INTGlnValValTTPargAsnThrAlaGluValGlyCysAlaGlnAlaSerCysAlaThr 182

[illegible][illegible]

C
C
C
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E
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C
C

DB EA709 11111
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Mon Feb 24 10:46:11 2003

us-09-832-320-2.p2n.rge

Page 16

Search completed: February 22, 2003, 03:42:25
Job time : 2068 secs

GenCore version 5.1.4.p5.4578
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OM nucleic - nucleic search, using sw model

Run on: February 22, 2003, 03:08:01 : Search time 233.123 seconds
(without alignments)
8674.789 Million cell updates/sec

Title: US-09-832-320-1

Perfect score: 898

Sequence: 1 ctcgcacgcacgcacgcgc.....aaaaaaaaaaaaaaaa 898

Scoring table: OLIGO_MDC
Gapop 60.0 , Gapext 60.0

Searched: 2185239 seqs, 1125999159 residues

Word size : 25

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Minimum DB seq length: 0

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Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	898	100.0	898	24	ABA96417
2	612	68.2	612	24	ABA96418
3	43	4.8	274	22	AAH35782
4	43	4.8	293	22	AAH71507
5	43	4.8	447	24	ABL93994
6	43	4.8	481	23	ABV58614
7	43	4.8	550	23	ABV57072
8	43	4.8	551	23	ABV56917
9	43	4.8	1077	22	AA527462

10	43	4.8	1091	22	AA899723	Maize ZmGn5N1-1 g1
11	43	4.8	1095	21	AACT77435	Human ORFX ORF290
12	43	4.8	1240	24	ABL01589	Human secreted pro
13	43	4.8	1483	22	AA504152	Human ras converti
14	43	4.8	1549	20	AA24921	Human ras carboxy-
15	43	4.8	1821	19	AAV59590	Human secreted pro
16	43	4.8	1835	20	AA27245	Human CLAR1 coding
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18	42	4.7	190	23	ABV20053	Human prostate exp
19	42	4.7	198	23	ABV55195	Human prostate exp
20	42	4.7	198	23	ABV5628	Human prostate exp
21	42	4.7	272	23	ABV18469	Human prostate exp
22	42	4.7	319	23	ABV49812	Human prostate exp
23	42	4.7	342	23	ABV46183	Human prostate exp
24	42	4.7	395	22	AA187795	Human polynucleoti
25	42	4.7	407	23	ABV58185	Human prostate exp
26	42	4.7	424	23	ABV55712	Human prostate exp
27	42	4.7	443	8	AAAT70773	Sequence encoding
28	42	4.7	456	22	AA183034	Human polynucleoti
29	42	4.7	464	23	ABV45981	Human prostate exp
30	42	4.7	465	23	ABV48253	Human prostate exp
31	42	4.7	495	22	ABV43074	Human breast cell
32	42	4.7	495	22	ABV53490	Human foetal liver
33	42	4.7	495	22	ABV23257	Probe #1723 for ge
34	42	4.7	495	22	ABV23257	Human brain expres
35	42	4.7	495	22	AAK27215	Human bone marrow
36	42	4.7	495	22	AA111796	Probe #1729 for ge
37	42	4.7	495	22	AA133110	Probe #1796 used t
38	42	4.7	495	22	AA101729	Probe #1720 used t
39	42	4.7	495	22	ABV01757	Human genome-deriv
40	42	4.7	595	24	AA501171	Fertilisation-lnde
41	42	4.7	707	22	AA525840	Human CDNA encodin
42	42	4.7	740	19	AAV23915	Plant CCR enzyme D
43	42	4.7	740	20	AA206881	Pine cinamoyl-CoA
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ALIGNMENTS

RESULT 1	ABA96417	standard; cDNA; 898 BP.
ID	ABA96417	
XX	ABA96417:	
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DT	02-APR-2002	(first entry)
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DE	Maize PRL-C10 encoding cDNA seq ID NO. 1.	
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KW	Maize; pathogen-related; PRL-C10; plant; transgenic; gene; ss.	
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OS	Zea mays.	
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EH		
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PD	06-DEC-2001.	
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FP	10-APR-2001; 2001US-0832320.	
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XX	10-APR-2000; 2000US-195801P.	
PR		
XX	(CRAN/) CRANE E H.	
PA	(CRAN/) CRANE V C.	
XX		
XX	Crane EH, Crane VC;	
PI		
XX		

DR WPI: 2002-121407/16.
P-PSDB: AAM48742.

xx New nucleic acid encoding a pathogen-related protein isolated from
PT maize and designated PRI-C10, useful for transforming plants for
PT enhanced disease resistance

xx Claim 1; Page 30-31; 34pp; English.

xx The invention relates to an isolated nucleic acid encoding a
CC pathogen-related protein PRI-C10. The nucleic acid is used to transform
CC plants for enhanced disease resistance.

xx Sequence 898 BP; 161 A; 295 C; 309 G; 133 T; 0 other;

Query Match 100.0%; Score 898; DB 24; Length 898;
Best Local Similarity 100.0%; Pred. No. 1.8e-288;
Matches 898; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 CAATGGGCGACTCGGAGGCGACACACCTCTCTGTCGCGGCGCCAGGCGCAACG 120
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QY 721 CGGCGGAGGCGGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 780
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DB 781 TTTTGT 840
QY 841 TCACCTTTTGT 898
DB 841 TCACCTTTTGT 898

RESULT 2

ID ABA96418 standard; cDNA; 612 BP.

AC ABA96418;

DT 02-APR-2002 (first entry)

DE Maize PRI-C10 coding sequence SEQ ID NO 3.

XX Maize; pathogen-related; PRI-C10; plant; transgenic; gene; ss.

OS Zea mays.

XX Key location/Qualifiers

FT CDS 1..612

FT /*tag= a

FT /product= "PRI-C10"

PN US2001049834-A1.

PD 06-DEC-2001.

PF 10-APR-2001; 2001US-0832320.

PR 10-APR-2000; 2000US-195801P.

PA (CRAN/) CRANE E. H.

PI (CRAN/) CRANE V C.

PS Crane EH, Crane VC;

DR WPI: 2002-121407/16.

DR P-PSDB: AAM48742.

PT New nucleic acid encoding a pathogen-related protein isolated from

PT maize and designated PRI-C10, useful for transforming plants for

PT enhanced disease resistance

PS Claim 1; Page 32; 34pp; English.

CC The invention relates to an isolated nucleic acid encoding a

CC pathogen-related protein PRI-C10. The nucleic acid is used to transform

CC plants for enhanced disease resistance.

CC Sequence 612 BP; 80 A; 231 C; 239 G; 62 T; 0 other;

QY Query Match 68.2%; Score 612; DB 24; Length 612;

QY Best Local Similarity 100.0%; Pred. No. 8.3e-194;

QY Matches 612; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 63 ATGGGCGACG 122

DB 1 ATGGGCGACG 60

QY 123 TGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 182

DB 61 TGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 120

QY 183 GCGGCTCTCATGCG 242

DB 121 CGGCTCTCTCATGCG 180

QY 243 AGCGGCGACG 302

DB 181 AGCGGCGACG 240

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Db	96	GGGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	54
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AC	ABL393994	(first entry)	
DE	Arabidopsis thaliana nucleic acid sequence Ref:2027755 SEQ ID NO:759.		
KW	Arabidopsis thaliana; insecticide; fungicide; plant; mapping; diagnosis;		
KW	genetic modification; gene; ss.		
OS	Arabidopsis thaliana.		
PN	US2002023280-A1.		
PD	21-FEB-2002.		
PR	26-JAN-2001; 2001US-0770444.		
PR	27-JAN-2000; 2000US-178502P.		
XX	(GORL/) GORLACH J.		
XX	(ANY/) AN Y.		
XX	(HAMT/) HAMILTON C M.		
XX	(PRIC/) PRICE J L.		
XX	(RAIN/) RAINES T M.		
XX	(YUY/) YU Y.		
XX	(RAME/) RAMEKA J G.		
XX	(PAGE/) PAGE A.		
XX	(MATH/) MATHEW A V.		
XX	(LEDF/) LEDFORD B L.		
XX	(WOES/) WOESSNER J P.		
XX	(HAAS/) HAAS W D.		
XX	(GARC/) GARCIA C A.		
XX	(KRIC/) KRICKER M.		
XX	(SLAF/) SLATER T.		
XX	(DAVI/) DAVIS K R.		
XX	(ALLE/) ALLEN K.		
XX	(HOEF/) HOFFMAN N.		
XX	(HORE/) HORBAN P.		
XX	Gorlach J, An Y, Hamilton CM, Price JL, Raines TM, Yu Y;		
XX	Rameka JG, Page A, Mathew AV, Ledford BL, Woessner JP, Haas WD;		
XX	Garcia CA, Kricker M, Slater T, Davis KR, Allen K, Hoffman N;		
XX	Hurban P;		
XX	WPI; 2002-267486/31.		
XX	New Arabidopsis thaliana nucleic acid, for identifying homologous		
XX	genes, producing compositions that modulate the expression or function		
XX	of its encoded protein, and mapping functional regions of a protein		
XX	Claim 1; SEQ ID 759; 447p; English.		

CC	physiological pathways. (1) can also be used; (1) for the genetic
CC	manipulation of cells, particularly plant cells; (2) in screening assays
CC	of various plant strains to determine the strains that are best capable
CC	of withstanding a particular disease or environmental stress; (3) for
CC	enhancing or inhibiting production of a biosynthetic product in a plant;
CC	(4) as probes in mapping and in diagnosis, in genetic modification and
CC	for screening purposes, to generate additional copies of the nucleic
CC	acids, to generate ribozymes or antisense oligonucleotides, and as
CC	single-stranded DNA probes or as triple-strand forming oligonucleotides;
CC	and (5) for generating genetically modified transgenic organisms.
CC	Note: The sequence data for this patent did not form part of the printed
CC	specification, but was obtained in electronic format directly from the
CC	USPTO web site.
XX	
SO	Sequence 447 BP; 123 A; 87 C; 68 G; 169 T; 0 other:
	Query Match 4.8%; Score 43; DB 24; Length 447;
	Best Local Similarity 100.0%; Pred. NO. 1.6e-05;
	Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0
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Dd	74 GGCTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 32
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DT	13-SEP-2002 (first entry)
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KM	Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
OS	pharmacogenomic marker; gene; ss.
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XN	Homo sapiens.
PN	MO200160860-A2.
PD	
XX	23-AUG-2001.
PF	
XX	20-FEB-2001; 2001MO-US05171.
PR	
PR	17-FEB-2000; 2000US-183319P.
PR	16-MAR-2000; 2000US-189862P.
PR	25-MAY-2000; 2000US-207454P.
PR	09-JUN-2000; 2000US-211314P.
PR	18-JUL-2000; 2000US-219007P.
PR	13-DEC-2000; 2000US-255281P.
PA	
XX	(MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
PI	
PI	Schlegel R, Endege WO, Monahan JE;
PI	WPI; 2001-662795/76.
DR	
XX	
XX	Novel isolated nucleic acid molecule associated with cancerous state of
PT	prostate cells and correlating with presence of prostate cancer, useful
PT	for detecting presence of prostate cancer, stage of prostate cancer -
XX	
XX	Claim 1; Page 1124/7; 11750pp; English.
PS	
XX	
CC	The invention relates to an isolated nucleic acid molecule (I) comprising
CC	a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC	specification or its complement. (I) is useful for:
CC	(a) assessing whether a patient is afflicted with prostate cancer;
CC	(b) monitoring the progression of prostate cancer in a patient;
CC	(c) assessing the efficacy of a test compound to inhibit prostate
CC	cancer in a patient;
CC	(d) assessing the efficacy of a therapy for inhibiting prostate cancer

CC in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound;
CC (g) determining whether prostate cancer has metastasized in a patient;
CC (h) assessing the aggressiveness or indolence of prostate cancer in a patient;
CC (i) is also useful as a pharmacodynamic or pharmacogenomic marker.
XX
SQ Sequence 481 BP; 186 A; 94 C; 92 G; 109 T; 0 other;
Query Match 4.8%; Score 43; DB 23; Length 481;
Best Local Similarity 100.0%; Pred. No. 1.6e-05;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 856 GCGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 898
DB 37 GCGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 79
RESULT 7
ABV57072/c
ID ABV57072 standard; cDNA; 550 BP.
XX
XX ABV57072;
AC
XX 17-SEP-2002 (first entry)
DT
XX
DE Human prostate expression marker cDNA 57063.
KW
XX Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW pharmacogenomic marker; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200160860-A2.
XX
PD 23-AUG-2001.
XX
PF 20-FEB-2001; 2001WO-US05171.
XX
PR 17-FEB-2000; 2000US-183319P.
PR 16-MAR-2000; 2000US-189862P.
PR 25-MAY-2000; 2000US-207454P.
PR 09-JUN-2000; 2000US-211314P.
PR 18-JUL-2000; 2000US-219007P.
PR 13-DEC-2000; 2000US-255281P.
XX
PA (MIL-) MILENNIUM PREDICTIVE MEDICINE INC.
XX
PI Schlegel R, Endege WO, Monahan JE;
XX
XX WPI; 2001-662795/76.
XX
XX Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer, stage of prostate cancer -
XX
XX Claim 1; Page 10986-10987; 11750pp; English.
XX
XX The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for:
CC (a) assessing whether a patient is afflicted with prostate cancer;
CC (b) monitoring the progression of prostate cancer in a patient;
CC (c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;
CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound;
CC (g) determining whether prostate cancer has metastasized in a patient;
CC (h) assessing the aggressiveness or indolence of prostate cancer in a patient;

CC (i) is also useful as a pharmacodynamic or pharmacogenomic marker.
XX
SQ Sequence 550 BP; 213 A; 169 C; 34 G; 134 T; 0 other;
Query Match 4.8%; Score 43; DB 23; Length 550;
Best Local Similarity 100.0%; Pred. No. 1.6e-05;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 856 GCGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 898
DB 145 GCGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 103
RESULT 8
ABV56917
ID ABV56917 standard; cDNA; 551 BP.
XX
XX ABV56917;
AC
XX 17-SEP-2002 (first entry)
DT
XX
DE Human prostate expression marker cDNA 56908.
KW
XX Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW pharmacogenomic marker; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200160860-A2.
XX
PD 23-AUG-2001.
XX
PF 20-FEB-2001; 2001WO-US05171.
XX
PR 17-FEB-2000; 2000US-183319P.
PR 16-MAR-2000; 2000US-189862P.
PR 25-MAY-2000; 2000US-207454P.
PR 09-JUN-2000; 2000US-211314P.
PR 18-JUL-2000; 2000US-219007P.
PR 13-DEC-2000; 2000US-255281P.
XX
PA (MIL-) MILENNIUM PREDICTIVE MEDICINE INC.
XX
PI Schlegel R, Endege WO, Monahan JE;
XX
XX WPI; 2001-662795/76.
XX
XX Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer, stage of prostate cancer -
XX
XX Claim 1; Page 10963-10964; 11750pp; English.
XX
XX The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for:
CC (a) assessing whether a patient is afflicted with prostate cancer;
CC (b) monitoring the progression of prostate cancer in a patient;
CC (c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;
CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound;
CC (g) determining whether prostate cancer has metastasized in a patient;
CC (h) assessing the aggressiveness or indolence of prostate cancer in a patient;
CC (i) is also useful as a pharmacodynamic or pharmacogenomic marker.
XX
SQ Sequence 551 BP; 238 A; 88 C; 74 G; 151 T; 0 other;
Query Match 4.8%; Score 43; DB 23; Length 551;
Best Local Similarity 100.0%; Pred. No. 1.6e-05;

Matches	43: Conservative	0: Mismatches	0: Indels	0: Gaps	0: Ambiguous
Oy	856 GGGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	898			
Db	110 GGGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	152			
RESULT 9					
ID	AA527462				
XX	AA527462 standard; cDNA; 1077 BP.				
XX	AA527462:				
XX	07-NOV-2001 (first entry)				
DE	cDNA encoding novel signal transduction pathway protein, Seq ID 497.				
XX					
KW	Neuroprotective; cytosolic; dermatological; immunosuppressive; tumour;				
KW	antiinflammatory; anti-HIV; antibacterial; antiinflammatory; cancer;				
KW	immune system disorder; Rheumatoid arthritis; inflammatory condition;				
KW	organ transplant rejection; infection; hepatitis C; blood disorder;				
KW	sickle cell anemia; hyperproliferative disorder; Gaucher's disease;				
KW	neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;				
KW	chromosomal abnormality; Down syndrome; ischaemia; renal disorder;				
KW	cardiovascular; respiratory; wound healing; endocrine; Addison's disease;				
KW	reproductive system; gastrointestinal; liver disorder; AIDS; SS;				
XX	acquired immune deficiency syndrome.				
XX	Homo sapiens.				
OS					
XX	MO200154733-A1.				
XX	02-AUG-2001.				
XX					
PF	17-JAN-2001; 2001MO-US01312.				
XX					
PR	31-JAN-2000; 2000US-0179065.				
PR	04-FEB-2000; 2000US-0180628.				
PR	24-FEB-2000; 2000US-0184664.				
PR	02-MAR-2000; 2000US-0186350.				
PR	16-MAR-2000; 2000US-0189874.				
PR	17-MAR-2000; 2000US-0190076.				
PR	18-APR-2000; 2000US-0198123.				
PR	19-MAY-2000; 2000US-0205515.				
PR	07-JUN-2000; 2000US-0209467.				
PR	28-JUN-2000; 2000US-0214886.				
PR	30-JUN-2000; 2000US-0215135.				
PR	07-JUL-2000; 2000US-0216647.				
PR	07-JUL-2000; 2000US-0216880.				
PR	11-JUL-2000; 2000US-0217487.				
PR	11-JUL-2000; 2000US-0217496.				
PR	14-JUL-2000; 2000US-0218290.				
PR	26-JUL-2000; 2000US-0220963.				
PR	26-JUL-2000; 2000US-0220964.				
PR	14-AUG-2000; 2000US-0224518.				
PR	14-AUG-2000; 2000US-0224519.				
PR	14-AUG-2000; 2000US-0225213.				
PR	14-AUG-2000; 2000US-0225214.				
PR	14-AUG-2000; 2000US-0225266.				
PR	14-AUG-2000; 2000US-0225267.				
PR	14-AUG-2000; 2000US-0225268.				
PR	14-AUG-2000; 2000US-0225270.				
PR	14-AUG-2000; 2000US-0225271.				
PR	14-AUG-2000; 2000US-0225277.				
PR	14-AUG-2000; 2000US-0225278.				
PR	14-AUG-2000; 2000US-0225279.				
PR	18-AUG-2000; 2000US-0226279.				
PR	22-AUG-2000; 2000US-0226581.				
PR	22-AUG-2000; 2000US-0226586.				
PR	22-AUG-2000; 2000US-0227182.				
PR	23-AUG-2000; 2000US-0227009.				
PR	30-AUG-2000; 2000US-0228924.				
PR	01-SEP-2000; 2000US-0229287.				

PR	01-SEP-2000	2000US-0229344
PR	01-SEP-2000	2000US-0229347
PR	01-SEP-2000	2000US-0229345
PR	05-SEP-2000	2000US-0229513
PR	05-SEP-2000	2000US-0229510
PR	06-SEP-2000	2000US-0230437
PR	06-SEP-2000	2000US-0230436
PR	08-SEP-2000	2000US-0231142
PR	08-SEP-2000	2000US-0231143
PR	08-SEP-2000	2000US-0231244
PR	08-SEP-2000	2000US-0231413
PR	08-SEP-2000	2000US-0231414
PR	08-SEP-2000	2000US-0232080
PR	08-SEP-2000	2000US-0232081
PR	12-SEP-2000	2000US-0231968
PR	14-SEP-2000	2000US-0232937
PR	14-SEP-2000	2000US-0232939
PR	14-SEP-2000	2000US-0233266
PR	14-SEP-2000	2000US-0233260
PR	14-SEP-2000	2000US-0233400
PR	14-SEP-2000	2000US-0233401
PR	14-SEP-2000	2000US-0233063
PR	14-SEP-2000	2000US-0233064
PR	14-SEP-2000	2000US-0233065
PR	21-SEP-2000	2000US-0234423
PR	21-SEP-2000	2000US-0234474
PR	25-SEP-2000	2000US-0234997
PR	25-SEP-2000	2000US-0234998
PR	25-SEP-2000	2000US-0234984
PR	25-SEP-2000	2000US-0234884
PR	27-SEP-2000	2000US-0235834
PR	27-SEP-2000	2000US-0235836
PR	29-SEP-2000	2000US-0236127
PR	29-SEP-2000	2000US-0236127
PR	29-SEP-2000	2000US-0236568
PR	29-SEP-2000	2000US-0236569
PR	29-SEP-2000	2000US-0236570
PR	29-SEP-2000	2000US-0236570
PR	02-OCT-2000	2000US-0238002
PR	02-OCT-2000	2000US-0237037
PR	02-OCT-2000	2000US-0237038
PR	02-OCT-2000	2000US-0237039
PR	02-OCT-2000	2000US-0237040
PR	13-OCT-2000	2000US-0239353
PR	13-OCT-2000	2000US-0239357
PR	13-OCT-2000	2000US-0239367
PR	20-OCT-2000	2000US-0241221
PR	20-OCT-2000	2000US-0241786
PR	20-OCT-2000	2000US-0241786
PR	20-OCT-2000	2000US-0241807
PR	20-OCT-2000	2000US-0241808
PR	20-OCT-2000	2000US-0241809
PR	20-OCT-2000	2000US-0241826
PR	01-NOV-2000	2000US-0244617
PR	01-NOV-2000	2000US-0244617
PR	08-NOV-2000	2000US-0246475
PR	08-NOV-2000	2000US-0246476
PR	08-NOV-2000	2000US-0246477
PR	08-NOV-2000	2000US-0246478
PR	08-NOV-2000	2000US-0246523
PR	08-NOV-2000	2000US-0246524
PR	08-NOV-2000	2000US-0246525
PR	08-NOV-2000	2000US-0246525
PR	08-NOV-2000	2000US-0246526
PR	08-NOV-2000	2000US-0246527
PR	08-NOV-2000	2000US-0246528
PR	08-NOV-2000	2000US-0246529
PR	08-NOV-2000	2000US-0246530
PR	08-NOV-2000	2000US-0246610
PR	08-NOV-2000	2000US-0246611
PR	08-NOV-2000	2000US-0246613
PR	17-NOV-2000	2000US-0249207
PR	17-NOV-2000	2000US-0249208
PR	17-NOV-2000	2000US-0249209
PR	17-NOV-2000	2000US-0249210
PR	17-NOV-2000	2000US-0249211
PR	17-NOV-2000	2000US-0249212

XX	Human ORF2990 polynucleotide sequence SEQ ID NO:5979.
DE	

KM Human; ven reading frame; ORFX detection; cytostatic; hepatocytic;
KM vulnerrary; antipsoiatric; antiparkinsonian; noctropic; neuroprotective;
KM anticoagulant; osteophytic; anfarthritis; immunosuppressant; cardiant;
KM immunostimulant; thrombolytic; coagulant; vasotropic; antiabiotic;
KM hypotensive; dermatological; immunosuppressive; antiinflammatory;
KM antiviral; antibacterial; antifungal; antihemmatic; antihypert;
KM antinaemic; gene therapy; cancer; proliferative disorder; hypertension;
KM neurodegenerative disorder; osteoarthritis; graft vs host disease;
KM cardiovascular disease; diabetes mellitus; hypochrydrol; SCID; AIDS;
KM cholesterol ester storage; systemic lupus erythematosus; infection;
KM severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
KM allergy; aplastic anaemia; nocturnal hemoglobinuria; burn; wound;
KM bone damage; cartilage damage; antiinflammatory disease; coagulation;
KM thrombosis; contraceptive; ss.

OS Homo sapiens.

PN W0200058473-A2.

PD 05-OCT-2000.

PF 31-MAR-2000; 2000WO-US08621.

PR 31-MAR-1999; 99US-0127607

05-APR-1999; 99US-0127728.

XX

(CONT.) CONGEN CONF:
FA
XX
XX

P1
XX

SILLIKELS RA,
LEACH R

DR WP1; 2000-602362/31.
DB P-PSDB: AABA3225.

Novel nucleic acids

PT useful for treating

XX
XX

XX

CC AAC774446 to AAC77606 encode the proteins given in AAB40237 to AAB43397.
CC These sequences represent the human OREX open reading frames 1 to 3161. The OREX
CC sequences have activities such as: cytostatic; hepatotropic; vulnary;
CC antiproliferative; antiparkinsonian; neurotrophic; neuroprotective;
CC osteopathologic; anticonvulsant; antiallergic; immunosuppressive;
CC immunostimulant; cardiact; thrombolytic; coagulant; vasotropic;
CC antidiabetic; hypotensive; dermatological; immunosuppressive;
CC antiinflammatory; antibacterial; antiviral; antifungal; antineumatic;
CC antithyroid; and antianemic. The sequences can be used for determining
CC the presence of or predisposition to, or preventing or treating
CC pathological conditions associated with an OREX-associated disorder. The
CC nucleic acids can be used to express OREX proteins in gene therapy.
CC vectors. The proteins and nucleic acids may be used to treat cancers,
CC proliferative disorders, neurodegenerative disorders, osteoarthritis,
CC graft vs host disease, cardiovascular disease, diabetes mellitus,
CC hypernatremia, hypothyroidism, cholesterol ester storage, systemic lupus
CC erythematosus, severe combined immunodeficiency (SCID), AIDS, viral,
CC bacterial or fungal infection, malaria, autoimmune disorders, asthma,
CC allergies, aplastic anaemia, burns, wounds, bone and cartilage damage,
CC nocturnal hemoglobinuria, antiinflammatory disease; to enhance
CC coagulation; to inhibit thrombosis; and as a contraceptive.

Sequence 1095 BP; 259 A; 333 C; 291 G; 210 T; 2 other;

Query Match	4.8%;	Score 43;	DB 21;	Length 1095;
Best Local Similarity	100.0%;	Pred. NO. 1.3e-05;		
Matches 43;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY 856 GGGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 898

Db 1034 GGCTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1076

RESULT 12	
ABL01589	
ID	ABL01589 standard; cDNA; 1240 BP

AC ABL01589

DT 15-MAR-2002 (first entry)

DE	Human secreted protein encoding polynucleotide SEQ ID NO 34

Human; nocitropic; neuroprotective; cytotoxic; dermatological; virocidic
 immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnereary;
 antiparkinsonian; atitchilling; antianaemic; antibrillifer; cancer;
 antihemetic; hepatotropic; cerebrotropic; antiinflammatory;
 antialergic; antidiabetic; antiserum; antitumor; antifungal;
 antiparasitic; cardiant; immune disorder; cardiovascular disorder;
 neurogenetic; disease; infection; neurotropic; gene therapy; vaccine; ss

OS Homo sapiens.

PN W0200183510-A1

PD 08-NOV-2001.

PF 26-APR-2001; 2001WO-US13318.

02-MAY-2000; 2000US-201194P
PR

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[illegible]

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F1
RESULTS OF, UNDER CM, UNDER CM,

DR WFL; 2002-121866/10
DR P-PSDB: ABB57417

XX
DT An isolated nucle

PT (SP) is useful in preventing, treating or ameliorating a disorder e.g. Alzheimer's disease and cancers -

XX 01416 10500 East 10th

PS Claim 1; Page 449; 496pp; English.

xx
CC The invention relates to novel genes (AB010566-ABL01594) and proteins
CC (ABB57394-ABB57456) useful for preventing, treating or ameliorating
CC medical conditions e.g. by protein or gene therapy. The genes are
CC isolated from a range of human tissues disclosed in the specification.
CC The nucleic acids, proteins, antibodies and (ant)agonists are useful
CC in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast
CC and ovarian cancer and other cancers of the adrenal gland, bone, bone
CC marrow, breast, gastrointestinal tract, liver lung, or urogenital;
CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune
CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative
CC colitis; (c) cardiovascular disorders such as myocardial ischaemias;
CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
CC and parasitic infections.

SQ Sequence 1240 BP; 303 A; 303 C; 403 G; 231 T; 0 other.

Query Match 4.8%; Score 43; DB 24; Length 1240;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

856 GGGTAAAAA 898

Db 1126 GGGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1168

RESULT 13

AA504152 standard; cDNA, 1483 BP.

AA504152;

24-OCT-2001 (first entry)

Human ras converting endoprotease (RCE) cDNA sequence.

Human; ras converting endoprotease; RCE inhibitor; placental; prenyl cysteine specific carboxymethyltransferase; cancer; ss.

Homo sapiens.

Key Location/Qualifiers
CDS 14..1003
/tag= a
/product= "RCE"

US6261793-B1.

17-JUL-2001.

04-MAR-1999; 99US-0262749.

04-MAR-1999; 99US-0262749.

(SCHE) SCHERING CORP.

Whyte D, McGuirk M, Nunez-Oliva I, Hockenberry T, Pat J;

WPI; 2001-450487/48.

P-PSDB; AAU03600.

Identifying human Ras Converting Endoprotease (RCE) inhibitors by

contacting radiolabelled prenylated protein with sample to be tested for

presence of inhibitor, and RCE, and measuring amount of labeled

tripeptide released -

Example 1; Column 13-16; 10pp; English.

The present sequence encoding for human ras converting endoprotease

(RCE) is isolated from a human placental cDNA library. RCE is used to

identify inhibitors of human RCE. Methods of identifying RCE inhibitors

comprises contacting a radiolabelled prenylated protein with the sample

to be tested for RCE inhibitors and RCE, and measuring the amount of

labelled tripeptide released; or contacting unlabelled prenylated

protein with the sample, RCE, prenyl cysteine specific

carboxymethyltransferase and radiolabelled methyl group donor (MD),

and measuring MD incorporated into the prenylated protein. The methods

of the invention are useful for identifying RCE inhibitors, which are

useful for treating cancer.

Sequence 1483 BP; 272 A; 448 C; 409 G; 354 T; 0 other;

Query Match 4.8%; Score 43; DB 22; Length 1483;

Best Local Similarity 100.0%; Pred. No. 1.2e-05;

Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

856 GGGTAAAAA 898

1430 GGGTAAAAA 1472

AAAX24921 standard; cDNA; 1549 BP.

AAAX24921;

05-JUL-1999 (first entry)

Human ras carboxy-terminal processing protein cDNA.

Ras carboxy-terminus processing protein; protease; human; cancer;

therapy; ss.

Homo sapiens.

Key Location/Qualifiers

CDS 6..1022

/tag= a

WO914343-A1.

25-MAR-1999.

18-SEP-1998; 98WO-US19746.

19-SEP-1997; 97US-0059401.

(ORTH) ORTHO-MCNEIL PHARM INC.

Chamberlain H, Farrell F, Galindo J, Huvar A, Johnson D;

Jolliffe L, Patel I;

WPI; 1999-229542/19.

P-PSDB; AAW98105.

New ras carboxyl terminal processing protein useful for identifying

modulators useful in therapy

Claim 2; Fig 1; 52pp; English.

This cDNA sequence encodes a novel human protein (see AAW98105)

that functions as a ras carboxyl terminal processing protein, and

optionally as a ras processing enzyme (i.e. ras protease). The

cDNA was cloned from a human colorectal adenocarcinoma cDNA

library following a homology search using yeast RCE1, the protease

responsible for ras processing in yeast. The cDNA has been

expressed in recombinant host cells which produce active

recombinant protein. The recombinant protein, and recombinant

host cells are utilised in a method for identifying modulators

of the enzyme activity, useful for treating a condition mediated

by activated ras protein. Inhibition of the human ras protease

should be efficacious for cancer treatment. Recombinant DNA

constructs, and portions of them, are useful for isolating

homologous sequences, identifying and isolating genomic

equivalents, and identifying, detecting or isolating mutant

forms of the ras carboxyl terminal processing protein DNA.

Sequence 1549 BP; 299 A; 440 C; 433 G; 374 T; 3 other;

Query Match 4.8%; Score 43; DB 20; Length 1549;

Best Local Similarity 100.0%; Pred. No. 1.2e-05;

Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

856 GGGTAAAAA 898

1448 GGGTAAAAA 1490

AAV59590 standard; DNA; 1821 BP.

AAV59590;

06-JAN-1999 (first entry)

Human secreted protein gene 80 clone HPWFL27.

Human; secreted protein; fusion protein; gene therapy; protein therapy;

diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukæmia;

developmental abnormality; foetal deficiency; blood; allergy; renal; ds;

KW immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
 KW inflammation; ischemic shock; Alzheimer's disease; restenosis; AIDS;
 KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
 KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
 KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
 XX Homo sapiens.
 XX W09839448-A2.
 XX 11-SEP-1998.
 XX 06-MAR-1998; 98WO-0504493.
 XX 02-OCT-1997; 97US-0061060.
 PR 07-MAR-1997; 97US-0038621.
 PR 07-MAR-1997; 97US-0040161.
 PR 07-MAR-1997; 97US-0040162.
 PR 07-MAR-1997; 97US-0040163.
 PR 07-MAR-1997; 97US-0040333.
 PR 07-MAR-1997; 97US-0040334.
 PR 07-MAR-1997; 97US-0040626.
 PR 11-APR-1997; 97US-0043311.
 PR 11-APR-1997; 97US-0043312.
 PR 11-APR-1997; 97US-0043313.
 PR 11-APR-1997; 97US-0043314.
 PR 11-APR-1997; 97US-0043568.
 PR 11-APR-1997; 97US-0043569.
 PR 11-APR-1997; 97US-0043576.
 PR 11-APR-1997; 97US-0043580.
 PR 11-APR-1997; 97US-0043669.
 PR 11-APR-1997; 97US-0043670.
 PR 11-APR-1997; 97US-0043671.
 PR 11-APR-1997; 97US-0043672.
 PR 11-APR-1997; 97US-0043674.
 PR 23-MAY-1997; 97US-0047492.
 PR 23-MAY-1997; 97US-0047500.
 PR 23-MAY-1997; 97US-0047501.
 PR 23-MAY-1997; 97US-0047502.
 PR 23-MAY-1997; 97US-0047503.
 PR 23-MAY-1997; 97US-0047581.
 PR 23-MAY-1997; 97US-0047582.
 PR 23-MAY-1997; 97US-0047583.
 PR 23-MAY-1997; 97US-0047584.
 PR 23-MAY-1997; 97US-0047585.
 PR 23-MAY-1997; 97US-0047586.
 PR 23-MAY-1997; 97US-0047587.
 PR 23-MAY-1997; 97US-0047588.
 PR 23-MAY-1997; 97US-0047589.
 PR 23-MAY-1997; 97US-0047590.
 PR 23-MAY-1997; 97US-0047592.
 PR 23-MAY-1997; 97US-0047593.
 PR 23-MAY-1997; 97US-0047594.
 PR 23-MAY-1997; 97US-0047595.
 PR 23-MAY-1997; 97US-0047596.
 PR 23-MAY-1997; 97US-0047597.
 PR 23-MAY-1997; 97US-0047598.
 PR 23-MAY-1997; 97US-0047599.
 PR 23-MAY-1997; 97US-0047600.
 PR 23-MAY-1997; 97US-0047601.
 PR 23-MAY-1997; 97US-0047612.
 PR 23-MAY-1997; 97US-0047613.
 PR 23-MAY-1997; 97US-0047614.
 PR 23-MAY-1997; 97US-0047615.
 PR 23-MAY-1997; 97US-0047616.
 PR 23-MAY-1997; 97US-0047617.
 PR 23-MAY-1997; 97US-0047618.
 PR 23-MAY-1997; 97US-0047632.
 PR 23-MAY-1997; 97US-0047633.
 PR 06-JUN-1997; 97US-0048964.
 PR 06-JUN-1997; 97US-0048974.
 PR 13-JUN-1997; 97US-0049610.

PR 08-JUL-1997; 97US-0051926.
 PR 16-JUL-1997; 97US-0052874.
 PR 18-AUG-1997; 97US-0053724.
 PR 22-AUG-1997; 97US-005630.
 PR 22-AUG-1997; 97US-005631.
 PR 22-AUG-1997; 97US-005632.
 PR 22-AUG-1997; 97US-005636.
 PR 22-AUG-1997; 97US-0056637.
 PR 22-AUG-1997; 97US-0056662.
 PR 22-AUG-1997; 97US-0056664.
 PR 22-AUG-1997; 97US-0056845.
 PR 22-AUG-1997; 97US-0056846.
 PR 22-AUG-1997; 97US-0056862.
 PR 22-AUG-1997; 97US-0056864.
 PR 22-AUG-1997; 97US-0056872.
 PR 22-AUG-1997; 97US-0056874.
 PR 22-AUG-1997; 97US-0056875.
 PR 22-AUG-1997; 97US-0056876.
 PR 22-AUG-1997; 97US-0056877.
 PR 22-AUG-1997; 97US-0056878.
 PR 22-AUG-1997; 97US-0056879.
 PR 22-AUG-1997; 97US-0056880.
 PR 22-AUG-1997; 97US-0056881.
 PR 22-AUG-1997; 97US-0056882.
 PR 22-AUG-1997; 97US-0056884.
 PR 22-AUG-1997; 97US-0056886.
 PR 22-AUG-1997; 97US-0056887.
 PR 22-AUG-1997; 97US-0056888.
 PR 22-AUG-1997; 97US-0056889.
 PR 22-AUG-1997; 97US-0056892.
 PR 22-AUG-1997; 97US-0056893.
 PR 22-AUG-1997; 97US-0056894.
 PR 22-AUG-1997; 97US-0056903.
 PR 22-AUG-1997; 97US-0056908.
 PR 22-AUG-1997; 97US-0056909.
 PR 22-AUG-1997; 97US-0056910.
 PR 22-AUG-1997; 97US-0056911.
 PR 05-SEP-1997; 97US-0057650.
 PR 05-SEP-1997; 97US-0057669.
 PR 05-SEP-1997; 97US-0057761.
 PR 12-SEP-1997; 97US-0058785.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX Bedharik DP, Brewer LA, Carter KC, Duan R, Ebner R, Endress GA;
 PI Feng P, Ferlie AM, Fischer CL, Florence RA, Greene JM, Hu JS;
 PI Kyaw H, Lafleur DW, Li Y, Moore PA, Ni J, Olsen HS, Rosen CA;
 PI Ruben SM, Shi Y, Soppet DR, Young PE, Yu GL, Zeng Z;
 XX WPI: 1998-506364/43.
 DR P-PSDB; AAW74810.
 XX
 PT New isolated human genes and the secreted polypeptide(s) they encode
 PT - useful for diagnosis and treatment of e.g. cancers, neurological
 PT disorders, immune diseases, inflammation or blood disorders
 XX
 PS
 XX Claim 1, Page 311-312; 721pp; English.
 CC This sequence represents a nucleic acid molecule designated Gene 80 from
 CC the human cDNA clone HMR27 (deposited as clone ATCC 97900 and ATCC
 CC 209046) which encodes a secreted human protein. The gene can be used to
 CC generate fusion proteins by linking to the gene to a human
 CC immunoglobulin Fc portion (e.g. AAV59502) for increasing the stability of
 CC the fused protein as compared to the human protein only.
 CC The invention relates to 186 novel genes and their fragments (nucleic
 CC acid sequences: AAV59511-V59812; amino acid sequences AAW74731-W75026)
 CC which are useful for preventing, treating or ameliorating medical
 CC conditions e.g. by protein or gene therapy. Also, pathological conditions
 CC can be diagnosed by determining the amount of the new polypeptides in a
 CC sample or by determining the presence of mutations in the new
 CC polynucleotides. Specific uses are described for each of the 186
 CC polynucleotides, based on which tissues they are most highly expressed in
 CC (see AAV59511 for described uses).

Sequence 1821 BP; 545 A; 429 C; 343 G; 497 T; 7 other;

Query Match 4.8%; Score 43; DB 19; Length 1821;

Best Local Similarity 100.0%; Pred. No. 1.1e-05;

Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 856 GCGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 898

Db 1661 GCGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1703

Search completed: February 22, 2003, 04:15:14
Job time : 248.123 secs

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 22, 2003, 03:42:31 ; Search time 1698.6 Seconds

(without alignments)
10485.621 Million cell updates/sec

Title: US-09-832-320-3

Perfect score: 612

Sequence: 1 atggcgcaactgcgcagcca.....aggcgcaagagccctactag 612

Scoring table: OLIGO_NTC

Gapop 60.0 , Gapext 60.0

Searched: 2054640 seqs, 14551402878 residues

Word size : 25

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : GenEmbl:*
1: gb.ba:*
2: gb.htg:*
3: gb.in:*
4: gb.om:*
5: gb.ov:*
6: gb.pat:*
7: gb.ph:*
8: gb.pl:*
9: gb.pr:*
10: gb.ro:*
11: gb.sts:*
12: gb.sy:*
13: gb.un:*
14: gb.vl:*
15: em.ba:*
16: em.fun:*
17: em.hum:*
18: em.in:*
19: em.mu:*
20: em.om:*
21: em.or:*
22: em.ov:*
23: em.pat:*
24: em.ph:*
25: em.pl:*
26: em.ro:*
27: em.sts:*
28: em.un:*
29: em.vl:*
30: em.htg.hum:*
31: em.htg.inv:*
32: em.htg.other:*
33: em.htg.mus:*
34: em.htg.pln:*
35: em.htg.rtd:*
36: em.htg.mam:*
37: em.htg.vrt:*
38: em.sy:*
39: em.htgo.hum:*
40: em.htgo.mus:*
41: em.htgo.other:*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40	6.5	144973	2	AC096689
2	40	6.5	150928	2	AC103550

ALIGNMENTS

RESULT 1
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LOCUS DEFINITION
Oryza sativa chromosome 3 clone OSJNBa0027J18, *** SEQUENCING IN
PROGRESS ***, 6 ordered pieces.
AC096689
AC096689 3 GI:18092993
VERSION
HTG, HTGS_PHASE2.
KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoidae; Oryzae; Oryza.

REFERENCE
AUTHORS
Buell, R., Hsiao, J., Zismann, V., Moffat, K.M., Hill, J.,
Gansberger, K., Burgess, S., Jarral, B., Shvartsbeyn, M., Brenner, M.,
Ciecko, A., Pal, G., Vanaken, S., Hansen, C., Ulterbach, T.,
Feildlyum, T., Khalak, H.G., Yuan, Q., Quackenbush, J., White, O.,
Salzberg, S. and Fraser, C.
Oryza sativa ssp. japonica cv. Nipponbare OSJNBa0027J18 BAC genomic
sequence
Unpublished
2 (bases 1 to 144973)
Buell, R.
Direct Submission
Submitted (22-SEP-2001) The Institute for Genomic Research, 9712
Medical Center Dr, Rockville, MD 20850, USA
On Jan 9, 2002 this sequence version replaced gi:17530731.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 6 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submitter.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
1 29894: contig of 29894 bp in length
29894: gap of unknown length
29995: contig of 40114 bp in length
70108: gap of unknown length
70109: contig of 9390 bp in length
70209: gap of unknown length
79598: contig of 26725 bp in length
79698: gap of unknown length
79699: contig of 106523 bp in length
106424: gap of unknown length
106523: contig of 33103 bp in length
106524: gap of unknown length
139627: contig of 5247 bp in length.
139727 144973: contig of 5247 bp in length.
Location/Qualifiers
1. 144973
/organism="Oryza sativa"
/cultivar="Nipponbare"
/sub_species="japonica"
/db_xref="taxon:4530"
/chromosome="3"
/clone="OSJNBa0027J18"

FEATURES

BASE COUNT 38927 a 32302 c 32466 g 40767 t 511 others
ORIGIN

Pred. No. is the number of results predicted by chance to have a

Query Match 6.5%; Score 40; DB 2; Length 144973;
Best Local Similarity 100.0%; Pred. No. 3.3e-08;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 571 TACAACCCGCGACGCAAGCTGCAGGCGCCAGCCCTACT 610
|||||
Db 136469 TACAACCCGCGACGCAAGCTGCAGGCGCCAGCCCTACT 136508

RESULT 2
AC103550/c
LOCUS 150928 bp DNA linear HTG 04-JUN-2002
DEFINITION Oryza sativa chromosome 3 clone OSJNBa0079G12, *** SEQUENCING IN
PROGRESS ***, 17 unordered pieces.
AC103550
AC103550.6 GI:21322019
HTG: HTGS_PHASE1.
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzoae; Oryza.
1 (bases 1 to 150928)
Buell, C.R., Yuan, Q., Ouyang, S., Liu, J., Tallon, L., Gansberger, K.,
Kim, M., Overton II, L., Bera, J., Tsiliris, T., Krol, M., Jarrohl, B.,
Jin, S., Koo, H., Zismann, V., Hsiao, J., Blunt, S., Vanaken, S.,
Unterbach, T., Feldblum, T., Yang, Q., Haas, B., Sub, B., Peterson, J.,
Quackenbush, J., White, O., Salzberg, S., and Fraser, C.
Oryza sativa ssp. japonica cv. Japonica cv. Nipponbare OSJNBa0079G12 BAC genomic
sequence
Unpublished
2 (bases 1 to 150928)
Buell, R.
Direct Submission
Submitted (27-NOV-2001) The Institute for Genomic Research, 9712
Medical Center Dr, Rockville, MD 20850, USA
3 (bases 1 to 150928)
Buell, R.
Direct Submission
Submitted (04-JUN-2002) The Institute for Genomic Research, 9712
Medical Center Dr, Rockville, MD 20850, USA
On Jun 4, 2002 this sequence version replaced gi:20153306.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 17 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 5616: contig of 5616 bp in length
* 5617 5663: gap of unknown length
* 5664 31941: contig of 26278 bp in length
* 31942 31988: gap of unknown length
* 31989 42994: contig of 11006 bp in length
* 42995 43041: gap of unknown length
* 43042 45430: contig of 2389 bp in length
* 45431 45477: gap of unknown length
* 45478 62104: contig of 16627 bp in length
* 62105 62151: gap of unknown length
* 62152 64960: contig of 2809 bp in length
* 64961 65007: gap of unknown length
* 65008 80503: contig of 15496 bp in length
* 80504 80550: gap of unknown length
* 80551 85002: contig of 4452 bp in length
* 85003 85048: gap of unknown length
* 85049 95622: contig of 10573 bp in length
* 95623 95669: gap of unknown length
* 95670 109958: contig of 14289 bp in length
* 109959 110005: gap of unknown length
* 110006 124211: contig of 14206 bp in length
* 124212 124258: gap of unknown length

124259 131728: contig of 7470 bp in length
* 131729 131775: gap of unknown length
* 131776 133914: contig of 2139 bp in length
* 133915 133961: gap of unknown length
* 133962 141548: contig of 7587 bp in length
* 141549 141595: gap of unknown length
* 141596 144303: contig of 2708 bp in length
* 144304 144349: gap of unknown length
* 144350 148834: contig of 4485 bp in length
* 148835 148880: gap of unknown length
* 148881 150928: contig of 2048 bp in length.

FEATURES
source
1. 150928
/organism="Oryza sativa"
/cultivar="Nipponbare"
/db_xref="taxon:4530"
/chromosome="3"
/clone="OSJNBa0079G12"
/note="japonica cultivar-group"
BASE COUNT 42065 a 34725 c 33029 g 40330 t 779 others
ORIGIN

Query Match 6.5%; Score 40; DB 2; Length 150928;
Best Local Similarity 100.0%; Pred. No. 3.3e-08;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 571 TACAACCCGCGACGCAAGCTGCAGGCGCCAGCCCTACT 610
|||||
Db 68225 TACAACCCGCGACGCAAGCTGCAGGCGCCAGCCCTACT 68186

Search completed: February 22, 2003, 05:29:30
Job time : 1908.6 secs